

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 24, 2004, 02:05:36 ; Search time 4190 Seconds

(without alignments)  
3783.123 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EAGSARPPPLLOEGWETVM 435

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q/cgn2.1/USPTO.spool/US09869565/runat.23112004.162645.29450/app.query.fasta\_1.583  
-DB=EST -QFMT=fastcap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USPR=US09869565@cgn.1.1.3437@runat.23112004.162645.29450 -ICPU=3  
-NO\_MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hcc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1874	82.1	2090	BC031578	BC031578 Homo sapi
2	1735.5	76.2	2009	CR595263	CR595263 full-leng
3	1510	66.1	1701	AY398834	AY398834 Mus muscu
4	1437	62.9	1035	BQ072459	BQ072459 AGENCOURT
5	1431	62.7	1037	5 BX381740	5 BX381740 AGENCOURT
6	1416	62.0	1707	9 AY398832	9 AY398832 Homo sapi
7	1401.5	61.4	929	6 CB183774	6 CB183774 AGENCOURT
8	1378	60.4	905	4 BG972488	4 BG972488 602841263
9	1337	58.6	876	4 B1102266	4 B1102266 602885578

10	1261	55.2	1051	7	CK231618	CK231618 ILLUMIGEN
11	1202.5	52.7	949	2	BF789775	BF789775 602105326
12	1197	52.4	898	5	BU219643	BU219643 603105084
13	1193	52.3	765	4	BG970555	BG970555 602838475
14	1182.5	51.8	710	6	CB600301	CB600301 AGENCOURT
15	1181.5	51.8	808	7	CK595861	CK595861 AGENCOURT
16	1177	51.6	952	4	BG828526	BG828526 602752641
17	1167.5	51.1	838	7	CK598594	CK598594 AGENCOURT
18	1106	48.4	667	1	AA575668	AA575668 VF64C10.1
19	1096	48.0	927	6	CB181376	CB181376 AGENCOURT
20	1075	47.1	751	6	CA945951	CA945951 UI-R-F50-
21	1071	46.9	944	6	CB203544	CB203544 AGENCOURT
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23	1033.5	45.3	827	1	AA987157	AA987157 uc81a02.x
24	1025	44.9	767	7	CO569702	CO569702 AGENCOURT
25	1012	44.3	713	6	CB322650	CB322650 UI-R-DY0-
26	1007	44.1	739	7	CK474354	CK474354 AGENCOURT
27	1006.5	44.1	2414	3	AK045576	AK045576 Mus muscu
28	968	42.4	701	1	AI327170	AI327170 mg54d06.x
29	965	42.3	1707	9	AY398833	AY398833 Pan trogl
30	962	42.1	553	2	BE101119	BE101119 UI-R-BU1-
31	942	41.3	556	2	BE749381	BE749381 200271 MA
32	939	41.1	608	2	BE294442	BE294442 601176049
33	933.5	40.9	925	5	BF980406	BF980406 602288296
34	926	40.6	539	5	BQ552052	BQ552052 H4013B06-
35	923	40.4	542	2	BE014986	BE014986 126918 MA
36	923	40.4	1647	2	BF782971	BF782971 602109056
37	918	40.2	540	2	BE749383	BE749383 200299 MA
38	905	39.6	653	5	BQ191730	BQ191730 UI-R-DY0-
39	902	39.5	517	1	AI409036	AI409036 EST237327
40	890	39.0	638	6	CA508167	CA508167 UI-R-F50-
41	870	38.1	662	6	CA508789	CA508789 UI-R-F50-
42	863.5	37.8	549	4	BG894790	BG894790 355529 MA
43	848.5	37.2	543	2	BF077875	BF077875 228051 MA
44	846.5	37.1	558	2	BF077876	BF077876 228052 MA
45	828	36.3	674	6	CA447251	CA447251 UI-H-E10-

ALIGNMENTS

RESULT 1  
BC031578  
LOCUS Homo sapiens parathyroid hormone receptor 1, mRNA (cDNA clone IMAGE:5180885), with apparent retained intron.  
DEFINITION BC031578 2090 bp mRNA linear HTC 01-APR-2004  
ACCESSION BC031578  
VERSION BC031578.1 GI:21618747  
KEYWORDS HTc.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2090)  
Straussberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,I., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worell,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,X.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences





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Db 1354 AGTGTACAGCTACCTCGGCCAACACACCGGGTGTGGGACTTGAGCTCGGGAAACAAAAAG 1413
QY 205 TTTTCTGAGTCTACCTCGGCCAACACACCGGGTGTGGGACTTGAGCTCGGGAAACAAAAAG 1413
Db 1414 TGGATCATCAGGTGCGCCATCTCTGCTCATTTGCTCAACTTCATCTCTTCAATCAAT 1473
QY 225 TTTTCTGAGTCTACCTCGGCCAACACACCGGGTGTGGGACTTGAGCTCGGGAAACAAAAAG 1413
Db 1474 ATCGTCCGGTGTGCTCGCCACCAAGTTCGGGAGACCAACCGCCGCGGTGTGACACACGG 1533
QY 245 GlnGlnTyrArgLysLeuLeuValLeuValLeuValLeuValLeuValLeuValLeuValHis 264
Db 1534 CAGCAGTACCGGAGTGTCTCAATCCACGCTGTGCTCATGCGCCCTCTTTGGCGTCCAC 1593
QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnLeuGln 284
Db 1594 TACATGCTTCATGGCCACCAATACCGAGCTCTCAGGGAGCGCTCTGCGAAGTCCAG 1653
QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaLalleleTyrCys 304
Db 1654 ATGCACCTATGAGATGCTCTTCACTCTCTCCAGGATTTTGTGCGAATCATATACTGT 1713
QY 305 PheCysAsnGlyGlnValGlnAlaGluLeuArgLysSerTrpSerArgTrpTrpLeuAla 324
Db 1714 TTTCTGCAATGGCAGGTACAGCTGAGATCAAGAAATCTTGAGCGCTGGACACTGGCA 1773
QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344
Db 1774 CTGGACTTCAGGCGAAGGACCGCAGCGGAGCAGAGCTATAGCTACGCGCCCATGGTG 1833
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
Db 1834 TCCACACAAAGTGTGACCAATGTGCGCCCGGTGGGACTCGGCTGCGCCCTCAGCCCC 1893
QY 365 Arg--LeuProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysPro 383
Db 1894 CGCCTACTGCCACTGCCACCTCTGCATAGTGGATGGACAGATGACCAAAAGAT 1953
QY 384 Gly 384
Db 1954 GGG 1956

RESULT 3
LOCUS AY398834
DEFINITION Mus musculus PTHR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY398834
VERSION AY398834.1 GI:39754823
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

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## FEATURES

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1. 1701  
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## ORIGIN

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Score: 1510.00 Matches: 286  
Percent Similarity: 91.69% Conservative: 1  
Best Local Similarity: 91.37% Mismatches: 26  
Query Match: 66.14% Indels: 0  
DB: 9 Gaps: 0

US-09-869-565-2 (1-435) x AY398834 (1-1701)

QY 123 AlaGlyCysArgValAlaValThrPheLeuTyrPheLeuAlaThrAsnTyrTrp 142  
Db 760 GCTGGCTGCGGTGGCGGTGACCTTCTCTCTACTTCTGCTGCTCACTACTACTGG 819  
QY 143 IleLeuValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPheSerGlyLys 162  
Db 820 ATTCTGGTGAGGAGCTGTACTTACACAGCCTCATCTTCTATGGCCTTTTCTCAGAGAAG 879  
QY 163 LysTyrLeuTyrGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaVal 182  
Db 880 AAGTATCTGTGGGGCTTCCACATCTTGGCTGGGNNNNNNNNNNNNNNNNNNNNNNNN 939  
QY 183 TrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHis 202  
Db 940 NNN 999  
QY 203 LysLysTrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPhelLeuPhe 222  
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QY 243 ThrArgGlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGly 262  
Db 1120 ACCAGCAGCAGTACCGAAGTGTCTCAGGTCCACGTTGGTGTCTTGGCCACTCTTCGGT 1179  
QY 263 ValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGln 282  
Db 1180 GTCCACTACCGCTCTTCATGGCTTCCGCTACACGAGGTCTCAGGACACTGTGGCAG 1239  
QY 283 IleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaLallele 302  
Db 1240 ATCCAGATGCATATGAGATGCTCTTCACTCTTCCAGGGATTTTGTGCGCATATA 1299  
QY 303 TyrCysPheCysAsnGlyGluValGlnAlaGluLeuArgLysSerTrpSerArgTrpThr 322  
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QY 323 LeuAlaLeuAspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyPro 342  
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QY 343 MetValSerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeu 362  
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QY 363 SerProArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLys 382  
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QY 383 ProGlyAlaProAlaThrGluThrLeuProValThrMetAlaValProLysAsp 402



Db 1540 CCGGGCGCTCCAGCATTTGAGACGAACCATACACGTTACTATGACAGTTCCTCCAGGAC 1599  
 Qy 403 AspGlyPheLeuAanGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArg 422  
 Db 1600 GACGGCTTCCTTAATGGCTCTGCTCGGGTCTGGATGAGGAGGCTCTGGGTCTGGCGG 1659  
 Qy 423 ProProProLeuLeuGlnGluGlyTrpGluThrValMet 435  
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## RESULT 4

BQ072459 1035 bp mRNA linear EST 02-APR-2002  
 LOCUS AGENCOURT\_6838764 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5761637  
 5', mRNA sequence.

ACCESSION BQ072459

VERSION BQ072459.1 GI:19901505

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1035)

NIH-MGC <http://mgc.nci.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L14M12810 row: j column: 06

High quality sequence start: 3

High quality sequence stop: 682.

## FEATURES

Location/Qualifiers  
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 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source  
 anonymous pool of 24 week female lung, 16 week female  
 spleen, and 20-22 week male spleens. Library is oligo-dT  
 primed and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.4 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 026. Note:  
 this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 9,62e-129 Length: 1035  
 Score: 1437.00 Matches: 278  
 Percent Similarity: 89.26% Conservative: 13  
 Best Local Similarity: 85.28% Mismatches: 29  
 Query Match: 62.94% Indels: 7  
 DB: 5 Gaps: 4

US-09-869-565-2 (1-435) x BQ072459 (1-1035)

Qy 112 ProProProAlaAlaAlaValGlyTyrAlaGlyCysArgValAlaValThrPhe 131  
 Db 23 CCCCCCGCGCTGCCACCGCGCTACCGGGCTGCAGGGTGGCTGTGACCTTC 82

Qy 132 PheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuValGluGlyLeuTyrLeuHis 151  
 Db 83 TTCCTTTACTTCTCCGGCCACCAACTACTACTTGGATTTCTGGTGGAGGGCTGTACTCGCAC 142  
 Qy 152 SerLeuIlePheMetAlaPhePheSerGlyLeuTyrLeuTyrGlyPheThrIlePhe 171  
 Db 143 AGCTCATCTTCATGGCTCTTCTCAGAGAAGAAGTACCTGTGGGGTTCACAGTCTTC 202  
 Qy 172 GlyTrpGlyLeuProAlaValPheValAlaValTrpValGlyValArgAlaThrLeuAla 191  
 Db 203 GGCCTGGGGTCTGGCCGCTGTCTCTGGCTGTGGGTTCAGTGTTCAGAGTACCTCCGCGCC 262  
 Qy 192 AsnThrGlyCysTrpAspLeuSerSerGlyHisTyrLeuTyrTrpIleIleGluValProIle 211  
 Db 263 AACACCGGGTCTGGGACTTTCAGCTCCGGGAACAAAAGTGGATCATCAGGTGGCCATC 322  
 Qy 212 LeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIleIleArgValLeuAlaThr 231  
 Db 323 CTGGCTTCATGTGCTCAACTTCTCTCATATATCGTCGGGTGTCCGCCACC 382  
 Qy 232 LysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArgLysLeuLeu 251  
 Db 383 AAGCTGCGGAGACCAACCGCGCGGTGTGCACACGCGCAGCAGTACCGGAAGTGTCTC 442  
 Qy 252 ArgSerThrLeuValLeuValProLeuPheGlyValHisTyrThrValPheMetAlaLeu 271  
 Db 443 AAATCCACGCTGGTGTCTATCCCTCTTTGGCGTCCACTACATTTGTTCTATGCGCCACA 502  
 Qy 272 ProTyrThrGluValSerGlyThrLeuTrpGlnIleGlnMetHisTyrGluMetLeuPhe 291  
 Db 503 CCATACACCGAGGTCTCAGGACGCTCTGGCAAGTCCAGATGCATCATGAGTGTCTTTC 562  
 Qy 292 AsnSerPheGlnGlyPhePheValAlaIleIleTyrCysPheCysAsnGlyGluValGln 311  
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 Qy 312 AlaGluIleArgLysSerTrpSerArgTrpThrLeuAlaLeuAspPheIleArgLysAla 331  
 Db 623 GCTGAGATCAAGAAATCTTGAGCGCTGGACACTGGCAGTGGACTTCAAGGGAAGGCA 682  
 Qy 332 ArgSerGlySerSerTyrSerTyrGlyProMetValSerHisThrSerValThrAsn 351  
 Db 683 CGCAGCGGAGCAGCAGCTATAGTACGCCCCCATGGTGTCCACACAGTGTGACCAAT 742  
 Qy 352 ValGlyProArgAlaGlyLeuSerLeuProLeuSerProArg---LeuProProAlaThr 370  
 Db 743 GTCGCCCCCGTGTGGGACTCGGCTGCCCTCAAGCCCCGCTACTGCCCACTGCCACC 802  
 Qy 371 ThrAsnGlyHisSerGlnLeuProGlyHisAlaLys-----ProGlyAlaProAlaThr 388  
 Db 803 ACCAAGCGCCACCTCAGCTGCGCCATGCCAAGGCCAGGACCCAGCCCCCTGGAGA- 861  
 Qy 389 GluThrGluThrLeuProValThrMetAlaValProLysAspAsp---GlyPheLeuAsn 407  
 Db 862 ACCTCGGAGACACACCACTGCCCTGCTCTCCCAAGGACCATGGGGTCTCTTCAAC 921  
 Qy 408 GlySerCysSer-GlyLeuAspGluAlaSerGlySerAlaArgProPro---ProIle 426  
 Db 922 GGTTCCTGCTCAAGGCTGGACCAAGAGCGCTTCTGGGCTTGAAGCGGCCCACTGCCCT 981  
 Qy 426 uLeuGlnGluGlyTrp 431  
 Db 982 GCTAAAGGAANAATGG 997  
 RESULT 5  
 LOCUS BX381740/c  
 DEFINITION BX381740 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 clone CS001069YC10 3-PRIME, mRNA sequence.  
 ACCESSION BX381740  
 VERSION BX381740.2 GI:46833542  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)



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ORIGIN
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Percent Similarity: 87.62% Conservative: 8
Best Local Similarity: 85.08% Mismatches: 37
Query Match: 62.02% Indels: 2
DB: 9 Gaps: 2

US-09-869-565-2 (1-435) x AV398832 (1-1707)

Qy 123 AlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTrp 142
Db 760 GCGGGCTGAGGGTGGCTGTGACCTTCTTCTTACTTCTTGGCCACCACTACTACTGG 819
Qy 143 IleLeuValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPheSerGluLys 162
Db 820 ATTCTGTGTGGAGGGCTGTACCTGCACAGCTCATCTTCTGTGCGCTTCTTCTCAGAGA 879
Qy 163 LysTyrLeuTyrGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaVal 182
Db 880 AAGTACCTGTGGGGCTTCCACAGTCTTCGGCTGGGNNNNNNNNNNNNNNNNNNNNNN 939
Qy 183 TrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHis 202
Db 940 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 999
Qy 203 LysLysTrpIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPhe 222
Db 1000 AAAAAGTGGATCATCCAGGTGCCATCTCTGGCTCCATTGTGCTCAACTTCATCTCTTC 1059
Qy 223 IleAsnIleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAsp 242
Db 1060 ATCAATATCGTCCGGGTGCTCGCCACCAAGCTGCGGGAGACCAACGCCGGCGGTGTGAC 1119
Qy 243 ThrArgGlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGly 262
Db 1120 ACAGCGACGAGTACCGAGAGCTGCTCAATCCAGCTGTGTGCTCATGCCCTCTTTGGC 1179
Qy 263 ValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGln 282
Db 1180 GTCCACTACATTGTCTTCATGGCCACACATACACCGAGGTCTCAGGAGCGCTCTGGCAA 1239
Qy 283 IleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIle 302
Db 1240 GTCCAGATGCATATGAGATGCTCTTCAACTCTCTTCCAGGGATTTTGTGCGCAATCAT 1299
Qy 303 TyrCysPheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThr 322
Db 1300 TACTGTTTCTGCAACGGCGAGGTACAGCTGAGATCAGAAATCTTGGAGCGCTGGACA 1359
Qy 323 LeuAlaLeuAspPheLysArgLysAlaAlaArgSerGlySerSerTyrSerTyrGlyPro 342
Db 1360 CTGGCACTGGACTTCAAGCGAAAGGACGACGCGGGAGCAGCAGCTATAGCTACGGCCCC 1419
Qy 343 MetValSerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeu 362
Db 1420 ATGGTGTCCCAACACAAAGTGTGACCAATGTGCGGCCCGCGTGTGGGACTCGGCCCTC 1479
Qy 363 SerProArg---LeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAla 381
Db 1480 AGCCCCCGCTACTGCCCCACTGCGCACCAACAGGCCACCTCAGCTGCTTGGCCATGCC 1539
Qy 382 LysProGlyAlaProAlaThrGluThr---GluThrLeuProValThrMetAlaValPro 400
Db 1540 AAGCCAGGGACCCCGAGCCCTGGAGACCCCTCGAGAGCACCAACACCTGCCATGGCTCTCC 1599

Qy 401 LysAspAspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySer 420
Db 1600 AAGGACGATGGGTTCTCAACGGCTCTCTCAGGCTCGGAGAGGAGGCTCTTGGGCT 1659
Qy 421 AlaArgProProProLeuLeuGlnGlyTrpGluThrValMet 435
Db 1660 GAGCGGCCCACTGGCTCTCTACAGGAGAGTGGGAGACAGTCAATG 1704

RESULT 7
LOCUS CB183774 929 bp mRNA linear EST 31-JAN-2003
DEFINITION AGENCOURT_11384721 NIH_MGC_164 Mus musculus cDNA clone
IMAGE:30244792 5', mRNA sequence.
ACCESSION CB183774
VERSION CB183774.1 GI:28182891
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 929)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. David Rowe and Dr. Mina
cDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloning Library: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDA00318 row: d column: 17
High quality sequence start: 2
High quality sequence stop: 590.
FEATURES
Location/Qualifiers
1..929
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30244792"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_164"
/notice="Vector: PCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;
Non-normalized full-length enriched library from pooled
mouse embryonic limb, maxilla and mandible, day 10.5 and
11.5 (size selected for the 0.5-1 kb fragments) Cloned
directionally, priming method: Oligo-dT. cDNA enrichment:
>1k bp, Average insert size 1.8k bp. Priming sequence:
5'-GACTAGTTCTAGATCGGAGCGGCCCTTT-3'. Tissue contributed
by, David Rowe. Library constructed by ResGen, Invitrogen
Corp."
ORIGIN
Alignment Scores:
Pred. No.: 2,31e-125 Length: 929
Score: 1401.50 Matches: 274
Percent Similarity: 98.21% Conservative: 1
Best Local Similarity: 97.86% Mismatches: 3
Query Match: 61.39% Indels: 2
DB: 6 Gaps: 1

US-09-869-565-2 (1-435) x CB183774 (1-929)

Qy 26 GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSer 45
Db 88 GAGTATTGTACCGCCCTGGGCGATGATCTACACCGTGGGATATTCATGTCTCTTGGCTCC 147
Qy 46 LeuThrValAlaValLeuLeuLeuAlaTyrPheArgArgLeuHisCysTyrArgAsnTyr 65
Db 148 CTCACCGTGGCTGTGCTCATCTAGCCCTATTTTAGCGGGCTGCACTCCACCGCACTAC 207

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Db      662  GGCCCCGTGAGGACTCAGCTTCCCTTAGCTCCGCGCTGC---TTCTGCACACCAAT 718
Qy      373  GlyHisSerGlnLeuProGlyHisAlaLysProGlyAlaProAlaThrGlu-ThrGluTh 392
Db      719  GGCCACTCCAGCTGCCTGGCCACGCCAAGCGGCGCTCCAGCCATTGAAGAACGAAC 778
Qy      392  rLeuProValThrMetAlaVal-ProLysAspAspGlyPheLeuAsnGlySerCysSerG 412
Db      779  CATACAGTTACTATGACAGTTCCTCCAAAGAGCAGCGGTTCTCTTTAATAGCTCTGCTCGG 838
Qy      412  lyLeuAsp---GluGluAlaSerGlySerAlaAatqProProProLeuLeuGlnGlu 429
Db      839  GTCTGGGATGAAGGAGGCTCTGGGTTGGCGGCAACCTCCATTGTTGGCGGNA 894

RESULT 9
LOCUS   B1102266
DEFINITION 602885578F1 NCI CGAP_Kid14 Mus musculus cDNA clone IMAGE:5040931
5' mRNA sequence.
ACCESSION B1102266
VERSION B1102266.1 GI:14553159
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 876)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.illnl.gov
Plate: LLAM1112 row: 1 column: 20
High quality sequence stop: 790.

FEATURES
source
1..876
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5040931"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Alignment Scores:
Pred. No.: 3.94e-119 Length: 876
Score: 1337.00 Matches: 272
Percent Similarity: 95.16% Conservative: 3
Best Local Similarity: 94.12% Mismatches: 6
Query Match: 58.56% Indels: 6
DB: 4 Gaps: 2

US-09-869-565-2 (1-435) x B1102266 (1-876)

Qy      26  GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSer 45
Db      10  GAGGTATTGTGACCGCTGGGATGATCATCACCGGGGATATTCATGCTCTTGCCCTCC 69
Qy      46  LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
Db      70  CTCACCGTGGCTGTGCTCATCTAGCCTATTATTAGCGGCTGCACTGACCGGCACTAC 129

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Qy      66  IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAsp 85
Db      130  ATCCACATGCACATGTTCTCTGCTTATGTGCGCGCGGAGCATCTTCGTGAAGGAC 189
Qy      86  AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGluLeu 105
Db      190  GCTGTGCTCTACTCTGGCTTCACGCTGGATGAGCGCGAGCGCTCCAGGAGAAAGATTG 249
Qy      106  HisIleIleAlaGlnValProProProAlaAlaAlaAlaValGlyTyrAlaGlyCys 125
Db      250  CATATCATCGCAGAGTGCCTCCACCGCGCTCCGCGCTGGCTACGCTGGCTGC 309
Qy      126  ArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrIleLeuVal 145
Db      310  CGTGTGGCTGTGACCTTCTCTACTTCTGGCTACCAACTACTACTGGATTCTGGTG 369
Qy      146  GluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysValTyrLeu 165
Db      370  GAGGACTGTACTTACACAGCTCACTTCATGCGCTTTTCTCAGAGAAGAAGTATCTG 429
Qy      166  TrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpValGly 185
Db      430  TGGGCTTCCACATCTTTGGCTGGGCTCTCGCGCTGCTTCGTGGCTGTGTGGTGGT 489
Qy      186  ValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTrp 205
Db      490  GTCAGAGCAACCTTGGCCAAACACTGGGTGCTGGGACCTGAGCTCTGGGCACAGAAGTG 549
Qy      206  IleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIle 225
Db      550  ATCATCCAGGTGCCCATCTGGCATCTGTGTGCTCAACTCTATCTCTTTATCAACATC 609
Qy      226  IleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGln 245
Db      610  ATCCGGGTGCTTGGCCACTAAGCTTCGGGAGACCAATGCGGCGCTGTGACACAGGCG 669
Qy      246  GlnTyrArgLysLeuLeuArgSer-ThrLeuValLeuValProLeuPheGlyValHisTyr 265
Db      670  CAGTACCGGAAAGCTGCTCAGGTCCACGCTGGTGTGCTTGGCCACTCTTCGGTGTCCA 729
Qy      265  r---ThrValPheMetAlaLeuProTyrThrGluValSerGlyThr-LeuTrpGlnIleG 284
Db      730  CCACGCTCTTCAATGGCTTGGCGGTACACGAGGTCTTCAGGGACACCTGTGGCAGATCC 789
Qy      284  InMetHisTyr-GluMetLeuPheAsnSerPheGlnGlyPheValAlaIleIleTyr 303
Db      790  AGATGGACTATTGAGATGCTCTTCAATCCTTCCAGG---ATTTTGTTGGCCATCATATC 846
Qy      304  CysPheCysAsnGlyGluVal 310
Db      847  GG-TTCTGCAAGGTGAAGGTG 866

RESULT 10
LOCUS   CK231618
DEFINITION ILLUMIGEN MCQ_2601 Katze MMLG Macaca mulatta cDNA 5' similar to
human PSG5 (Hs.251850), mRNA sequence.
ACCESSION CK231618
VERSION CK231618.1 GI:39637976
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Macaca.
1 (bases 1 to 1051)
Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magness,C.L.
Large-scale Rhesus Macaque cDNA Sequencing
Unpublished (2003)
Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

```

Tel: 2063780400  
 Fax: 2063780408  
 Email: cmagness@illumigen.com  
 Sequenced on 2003.10.29. 784 Q20 bases. Assemblies in contig w/ 121 member(s). Contig contains 26 (5.2%) lib members.

PCR Primers  
 FORWARD: CCTCACTAAAGGGAACAAA  
 BACKWARD: CACTATAGGCGAATGGTA  
 Insert length: 1051 Std Error: 0.00  
 Plate: CL000022 row: H column: 08  
 Seq primer: CCTCACTAAAGGGAACAAA  
 POLYA=Yes.

## FEATURES

source  
 1..1051  
 /organism="Macaca mulatta"  
 /mol\_type="mRNA"  
 /strain="Indian"  
 /db\_xref="taxon:9544"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="E. coli SOLR"  
 /clone\_lib="Ratze WMLG"  
 /note="Organ: lung; Vector: Uni-ZAP XR; Site 1: Ecor I;  
 Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis  
 kit (Catalog #200400) and ZAP-cDNA Gigapack III Gold  
 Cloning Kit (Catalog #200450)"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,26e-111 Length: 1051  
 Score: 1261.00 Matches: 241  
 Percent Similarity: 92.91% Conservative: 8  
 Best Local Similarity: 89.93% Mismatches: 16  
 Query Match: 55.23% Indels: 3  
 DB: 7 Gaps: 2

US-09-869-565-2 (1-435) x CK231618 (1-1051)

QY 171 PheGlyTrpGlyLeuProAlaValPheValAlaValTrpValGlyValAlaArgAlaThrLeu 190  
 Db 3 TTCGGTGGGGTCTGCCCGCTGCTTGGTGGCTGTGGTGGTCACTGTCAGAGTACCGCTG 62  
 QY 191 AlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTrpIleLeuGlnValPro 210  
 Db 63 GCCAACACCGGGTCTGGGACTGAGCTCCGGGAACAAAAGTGGATCATCCAGGTGCC 122  
 QY 211 IleLeuAlaSerValValLeuAsnPhelLeuPheIleAsnIleLeuArgValLeuAla 230  
 Db 123 ATCTGGCTTCCATGTGCTCAACTTCATCTCTTCATCAATATCGTCCGGGTGCTGCC 182  
 QY 231 ThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArgLysLeu 250  
 Db 183 ACCAAGTGGGAGACCAACGCTGGCGGTGTGACACGGCGGACGAGTACCGGAAGCTG 242  
 QY 251 LeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyrThrValPheMetAla 270  
 Db 243 CTCAAATCCACGCTGGTCTCATGCCCTCTTTGGCGTCCACTACATCGTCTTCATGGCC 302  
 QY 271 LeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGlnMetHisTyrGluMetLeu 290  
 Db 303 ACACCATACACCGAGGTCTCAGGAGCGCTCTGGCAAGTCCAGATGCATATGAGATGCTC 362  
 QY 291 PheAsnSerPheGlnGlyPheValAlaIleIleTyrCysPheCysAsnGlyGluVal 310  
 Db 363 TTCAACTCTTCAGGAGATTTTGTGCGCATCATATACGTGTTCTTGCAATGGCGAGTA 422  
 QY 311 GlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAlaLeuAspPheLysArgLys 330  
 Db 423 CAAGCTGAGATCAAGAAATCTTGAGCGGTGGACACTGGCACTGGACTTCAAGCGCAAG 482  
 QY 331 AlaArgSerGlySerSerTyrSerTyrGlyProMetValSerHisThrSerValThr 350  
 Db 483 GCACGCGAGCGGAGCAGCAGTATAGTATGCGCCCATGTGTGCCACACAAAGTGTGACC 542

QY 351 AsnValGlyProArgAlaGlyLeuSerLeuProLeuSerProArg----LeuProProAla 369  
 Db 543 AACGTGCGCGCGGTGTGGACTCGGCTCCCTCCCTCAGCCCGCCCTACTGCCACTGCC 602  
 QY 370 ThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGlyAlaProAlaThrGlu 389  
 Db 603 ACCACCATGGCCACCTCAGCTGCTGGCCATGCCAAGCCAGGGGCCCGAGCCCTGGAG 662  
 QY 390 Thr---GluThrLeuProValThrMetAlaValProLysAspAspGlyPheLeuAsnGly 408  
 Db 663 ACCCTCGAGACCACACCCTCGCTGGTGTCTCCCAAGGACGATGGTTCCTCAACGGC 722  
 QY 409 SerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProProProLeuLeuGlu 428  
 Db 723 TCCTGCTCGGGCTGGACGAGGAGGCTCTGGGCCCTGAGCGGCCACCCCGCTGCTACA 782  
 QY 428 nGluGlyTrpGluThrValMet 435  
 Db 783 GGAAGAGTGGGACAGATCATG 804

## RESULT 11

BF789775 949 bp mRNA linear EST 12-JAN-2001  
 LOCUS 602105326F1 NCI\_CGAP\_Kid14 Mus musculus cDNA clone IMAGE:4223190  
 DEFINITION 5' mRNA sequence.

ACCESSION BF789775 GI:12094811

VERSION BF789775 EST.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 949)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM9811 row: d column: 07  
 High quality sequence stop: 683.

## FEATURES

source

1..949  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4223190"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI\_CGAP\_Kid14"  
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.75 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library. |"

## ORIGIN

Alignment Scores:  
 Pred. No.: 5,24e-106 Length: 949  
 Score: 1202.50 Matches: 251  
 Percent Similarity: 83.17% Conservative: 6  
 Best Local Similarity: 81.23% Mismatches: 17  
 Query Match: 52.67% Indels: 36  
 DB: 2 Gaps: 5

US-09-869-565-2 (1-435) x BF789775 (1-949)

QY 58 ArgLeuHisCysThrArgAsnTyrIleHisMetHisMet-PheLeuSerPheMetLeuAr 77  
 Db 3 CGGCTGCATGTCACGCGCAACTACATCCACATGCATGGTTCCCTGTCTTATCTCGC 62  
 QY 77 GAlaAlaSerIlePheValLysAspAlaValLeuTyrSerGlyPheThrLeuAspGluAl 97  
 Db 63 CGCCGCGAGCATCTTCGTGAGGAGCGTGTCTTACTCTGTGCTTACGCTGGAATGAGC 122  
 QY 97 aGluArgLeuThrGluGluGluLeuHisIleIleAlaGlnValProProProAlaAl 117  
 Db 123 CGAGCGCTCACCGAGGAAGAGTTGCATATCATCGCGCAGGTGCGCTCCACCGCGCGC 182  
 QY 117 aAlaAlaValGlyTyrAlaGlyCysArgValAlaValThrPheLeuTyrPheLeuAl 137  
 Db 183 TGCCCGCGTGTGCTACGCTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCG 242  
 QY 137 aThrAsnTyrTyrTrpIleLeuValGluGluLeuTyrLeuHisSerLeuIlePheMetAl 157  
 Db 243 TACCAACTACTACTGATCTGCTGAGGAGCTGTACTTACACGCTCACTTCATGCGC 302  
 QY 157 aPhePheSerGluLysLysTyrLeuTrpGlyPheThrIlePheGlyTyrGlyLeuProAl 177  
 Db 303 CTTTTTCTCAGAGAAGAGTATCTGTGGGCTTCACCATCTTTGGCTGGGGTCTGCCGCGC 362  
 QY 177 aValPheValAlaValTrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAs 197  
 Db 363 TGTCTCTGCGGTGCTGTGGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTG 422  
 QY 197 PleuSerSerGlyHisLysLysTyrTrpIleGlnValProIleLeuAlaSerValValle 217  
 Db 423 CTGTGAGCTCTGGCACAGAGTGTATCATCAGGTGCCATCTGTGCTGTGTGTGTGTGT 482  
 QY 217 uAsnPheIleLeuPheIleAsnIleArgValLeuAlaThrLysLeuArgGluThrAs 237  
 Db 483 CAACCTTCATCTCTTTATCAACATCATCGGGTGTCTTGCACCTAAGCTTCGGGAGACAA 542  
 QY 237 nAlaGlyArgCysAspThrArgGlnTyrArgLysLeuLeuArgSerThrLeuValle 257  
 Db 543 TGCGGGCGGTGTGACACGAGCAGTACCGGAAGTGTCTGAGGTCCACGTTCAGGTGTGT 602  
 QY 257 uValProLeuPheGlyValHisTyrThrValPheMetAlaLeuProTyrThrGluValSe 277  
 Db 603 TGTGCACTCTTCGTGTCCATACACGCTTTCATGGCTTGCCTGCGGTACACA--GTCTC 660  
 QY 277 rGlyThrLeuTrpGlnIleGln---MetHisTyrGluMetLeuPheAsnSerPheGlnGl 296  
 Db 661 AGGACACTGTGGCAGATCCAGATGCCCTATTAGAAATGCTCTTCAACTCCTTCAGGG 720  
 QY 296 yPhePheValAlaIleIleTyrCysPheCysAsnGlyGluValGlnAlaGluIleArgLy 316  
 Db 721 ATTTTTTGTGGCGCTCATA-----GCATGGTGGTGGTGGTGGTGGTGGTGGTGG 739  
 QY 316 sSerTrpSerArgTrpThrLeuAlaLeuAspPheLysArgLysAlaArgSerGlySerSe 336  
 Db 740 -TCCTGGTCT-----GCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 766  
 QY 336 rSerTyrSerTyrGlyProMetValSerHisThrSerValThrAsnValGlyProArg-- 355  
 Db 767 -----CCAAATTTGAAGTCTGTGGCGCTGACCTGGTGGTGGTGGTGGTGGTGG 810  
 QY 356 -----AlaGlyLeuSerPro 361  
 Db 811 AACCAAGTGGGTGACTTCTATTTCCC 835  
 RESULT 12  
 BU219643  
 LOCUS  
 DEFINITION 603105084F1 CSEQCHN04 Gallus gallus cDNA clone ChEST42h21 5', mRNA  
 sequence.  
 ACCESSION BU219643  
 VERSION BU219643.1 GI:25404449  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)

## ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ruteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

## REFERENCE

1 (bases 1 to 898)

## AUTHORS

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)

## JOURNAL

2235534

## MEDLINE

12445392

## COMMENT

Contact: Simon Hubbard

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Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

Location/Qualifiers

1..898

/organism="Gallus gallus"

/mol\_type="mRNA"

/strains="White Leghorn, Hisex"

/db\_xref="taxon:9031"

/clone="ChEST42h21"

/tissue\_type="whole embryo"

/dev\_stage="20-21"

/lab\_host="DH10B"

/clone\_lib="CSEQCHN04"

/note="Organ: whole embryo; Vector: pBluescript II KS(+);

Site 1: EcoRI; Site 2: NotI; This normalized library was

constructed from 1 million independent clones. cDNA

synthesis was initiated using an oligo(dT) primer, using

methylated C in the first strand synthesis reaction.

Following this first strand reaction, double-stranded cDNA

was blunted, ligated to NotI adapters, digested with

EcoRI, size-selected, and cloned into the NotI and EcoRI

compatible sites of a custom modified MCS of the

pBluescript (KS+) vector. The library was normalized in 2

rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bernaldo et al., Genome Research 6

(1996): 791, except that a significantly longer

reannealing hybridization was used."

## ORIGIN

Alignment Scores:

Pred. No.: 1,65e-105 Length: 898

Score: 1197.00 Matches: 233

Percent Similarity: 88.01% Conservative: 24

Best Local Similarity: 79.79% Mismatches: 30

Query Match: 52.43% Indels: 6

DB: 5 Gaps: 1

US-09-869-565-2 (1-435) x BU219643 (1-898)

QY 73 SerPheMetLeuArgAlaAlaSerIlePheValLysAspAlaValLeuTyrSerGlyPhe 92

Db 5 TCCTTCATGTTGAGAGCTGTGAGCATCTCGTGAAGGACGCGGTCTTATCTCTGGTCA 64

QY 93 ThrLeuAspGluAlaGluArgLeuThrGluGluLeuHisIleAlaGlnValPro 112

Db 65 GCTTTGGAGGAGATGGAGCGGATTTCTGAGGAAGACCTGGAATCCATTAACGAACACCT 124

QY 113 ProProAlaAlaAlaAlaValGlyTyrAlaGlyCysArgValAlaValThrPhePhe 132

Db 125 CCA-----GCAGATAAGTCACAGTTGTGGGTTCGAAAGTAGCGGTACTTCTTC 175

QY 133 LeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuValGluGlyLeuTyrLeuHisSer 152

Db 176 CTCTACTTCTCTGGCAACCAATTACTACTGTGATTCGTGGAAGGGCTCTATCTCCACAGC 235

QY 153 LeuIlePheMetAlaPhePheSerGluLysLysTyrLeuTrpGlyPheThrIlePheGly 172

```

Db      236  CTCATCTTCATGGCTTTTCTCAGAGAGAGATCTTTGGGATTCACATATTATTTGGC 295
Qy      173  TrpGlyLeuProAlaValPheValAlaValTrpValGlyValAlaValArgAlaThrLeuAlaAsn 192
Db      296  TGGGGACTCCCTGCTGTATTGTTACAGCGCTGGCGCCAGCGGTGAGAGCCACTCTAGCTGAC 355
Qy      193  ThrGlyCysTrpAspLeuSerGlyHisIlyslsYsrPrllelleGlnValProIleIeu 212
Db      356  ACAGAGTGTGGGACTTGAGCTGGCAATTTAAATGGATTTATTCAGGTGCCCATCTG 415
Qy      213  AlaSerValValLeuAsnPheIleLeuPheIleAsnIlelleArgValLeuAlaThrLys 232
Db      416  GCAGCTATCGTGGTAAATTTATTTCTTTTATCAATATATCAGAGCTCTAGCAACCAAG 475
Qy      233  LeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArgLysLeuLeuArg 252
Db      476  CTACGGGAAACAAATGACGGAGGTGTGACTCAGCAGAACAGTACAGGAAGCTGCTGAAA 535
Qy      253  SerThrLeuValLeuValProLeuPheGlyValHisTyrThrValPheMetAlaLeuPro 272
Db      536  TCTACCTCTGCTCTATGCTCTGTTTGGCGTTTCACTATATGTTTTCATGGCTATGCCA 595
Qy      273  TyrThrGluValSerGlyThrLeuTrpGlnIleGlnMetHisTyrGluMetLeuPheAsn 292
Db      596  TACACAGATGTGCAGGATCTTGGGCAAGTTCAAATGCACATATGAATGCTGTCTTCAAC 655
Qy      293  SerPheGlnGlyPhePheValAlaIlelleTyrCysPheCysAsnGlyGluValGlnAla 312
Db      656  TCTTTCAGGGATTTTGTGGCCATCATATACCTATGTTTTCATGAGAGGTCCAAGCA 715
Qy      313  GluIleArgLysSerTrpSerArg-TrpThrLeuAlaLeuAspPhe-LysArgLysAlaA 332
Db      716  GAAATAAGAGATCATGACAGCGGTGGACATTAGCACTTGATTTTAAAGAGGAACAC 775
Qy      332  rgSerGlySerSerTyrSerTyrGlyProMetValSerHisThrSerValThrAsnV 352
Db      776  GAAAGTGGAGCACACCTACAGTATGACCAATGTTCCACAGCAAGCATCAACAATG 835
Qy      352  alGlyProArgAlaGlyLeuSerLeuProLeu 362
Db      836  TAGC-CCGAGAGGGGCACCTTGGGCTCCATCTC 866

BG970555 765 bp mRNA linear EST 12-JUN-2001
602838475F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4972795
5', mRNA sequence.
BG970555
BG970555.1 GI:14358192
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@lemail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M10960 row: e column: 20
High quality sequence stop: 741.
Location/Qualifiers
1..765
/organism="Mus musculus"

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/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
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/notes="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"

ORIGIN
Alignment Scores:
Pred. No.: 3.19e-105 Length: 765
Score: 1193.00 Matches: 250
Percent Similarity: 96.15% Conservative: 0
Best Local Similarity: 96.15% Mismatches: 2
Query Match: 52.26% Indels: 9
DB: 4 Gaps: 0

US-09-869-565-2 (1-435) x BG970555 (1-765)

Qy      51  LeuIleLeuAlaTyrPheArgArg-LeuHisCysThrArgAsnTyrIleHisMetHisMe 70
Db      3  CTCATCTTCATGGCTTTTCTCAGAGAGAGATCTTTGGGATTCACATATTATTTGGC 62
Qy      70  tPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAspAlaValLeuTyrSe 90
Db      63  GTTCCTGTCTGTATGCTGCGCGCCGAGCATCTTCGTGAAGACACCTGTGCTCTACTC 122
Qy      90  rGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGluLeuHisIlelleAlaGl 110
Db      123  TGCGTTTTCATGGCTTTTCTCAGAGAGAGATCTTTGGGATTCACATATTATTTGGC 182
Qy      110  nValProProProAlaAlaAlaValGlyTyrAlaGlyCysArgValAlaValTh 130
Db      183  GGTGGCGCTCCACCGCGCTGCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 242
Qy      130  rPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuValGluGlyLeuTyrLe 150
Db      243  CTTCCTCTCTACTTCTGCTACCACTACTTCTGATTTCTGGTGGAGGAGTGTACTT 302
Qy      150  uHisSerLeuIlePheMetAlaPhePheSerGluLysLysTyrLeuTrpGlyPheThrI 170
Db      303  ACACAGCTTCATCTTTCATGGCTTTTCTCAGAGAGAGATCTTTGGGATTCACCAT 362
Qy      170  ePheGlyTrpGlyLeuProAlaValPheValAlaValTrpValGlyValArgAlaThrLe 190
Db      363  CTTTGGCTGGGCTCTGCGGCTGTCTGCTGGCTGTGCTGGCTGTGCTGGCTGTGCTG 422
Qy      190  uAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTrpIlelleGlnValPr 210
Db      423  GGCACACATCTGGGTGGTGGGACCTGAGCTCTGGGCAACAAGTGGATCATCCAGGTGC 482
Qy      210  olleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIlelleArgValLeuAl 230
Db      483  CATCTTGGCATCTGTTGTGCTCACTTCATCTCTTTATCAACATCATCCGGGTGCTTGC 542
Qy      230  aThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArg-LysL 250
Db      543  CACTAAGCTTCGGGAGACCAATCGGCGCGCTGTGACACCCAGGAGCAGTACCGCGAAGC 602
Qy      250  euLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyrThrVal-PheMet 269
Db      603  TGCTCAGTCCACGTTGGTCTGTGCGCACTCTTCGCTGTGCTGTGCTGTGCTGTGCTG 662
Qy      270  Ala-LeuProTyrThrGluValSerGlyThrLeu-TrpGlnIleGln-MetHisTyrGlu 288
Db      663  GCCCTTGGCGTACACCGAGGTCTCAGGACACCTGTTGGCAGATCCAGATGCATATGAG 722
Qy      289  -MetLeu-PheAsnSerPheGlnGlyPhePheValAlaIlelle 302
Db      723  AATGCTCTTTCAACTCTTCCAGGATTCGTG-TGAGCCATCAT 765

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RESULT 14
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LOCUS
DEFINITION AGENCOURT 13041423 NIH_MGC 176 Mus musculus cDNA clone
IMAGE:30311807 5', mRNA sequence.
ACCESSION CB600301
VERSION CB600301.1 GI:29518157
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 710)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: NDCM95 row: 1 column: 24
High quality sequence stop: 636.
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1..710
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30311807"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_176"
/notes="Organ: kidney; Vector: pDNR-LIB; Site 1: SfiI
(ggcatatggccc); Site 2: SfiI (ggcgctcgccc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTACACGACGATGGCATTACGGCGGG-3' and
5'-ATTCTAGCGCGGCGGCGGACATG-dt(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 2,99e-104 Length: 710
Score: 1182.50 Matches: 225
Percent Similarity: 96.58% Conservative: 1
Best Local Similarity: 96.15% Mismatches: 7
Query Match: 51.80% Indels: 1
DB: 6 Gaps: 1

US-09-869-565-2 (1-435) x CB600301 (1-710)

QY 133 LeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuValGluGlyLeuTyrLeuHisSer 152
Db 4 CTCCTACTTCCTGGCTACCACTACTCTGGATTCCTGGTGGAGGACTGTACTTACACAGC 63

QY 153 LeuIlePheMetAlaPhePheSerGluIlystysTyrLeuTyrGlyPheThrIlePheGly 172
Db 64 CTCATCTTCATGGCCTTTTCTCAGAGAAGATATCTGTGGGGCTTCACCATCTTTGGC 123

QY 173 TrpGlyLeuProAlaValPheValAlaValTrpValGlyValArgAlaThrLeuAlaAsn 192
Db 124 TGGGGTCTGCCGGCTGTCTTCGTGGGTGTGTGGGTGTGTGGGTGTGTGGGTGTGTGGGT 183

QY 193 ThrGlyCysTrpAspLeuSerSerGlyHisIlystysTyrTrpIleGlnValProIleLeu 212
Db 184 ACTGGGTGTCTGGGACCTGAGCTCTGGGCAAGAAGTGGATCATCGGTGCCATCCTG 243

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QY 213 AlaSerValValLeuAsnPheIleLeuPheIleAsnIleIleArgValLeuAlaThrIlys 232
Db 244 GCATCTGTGTGTGCTCAACTCTCTTTATCAACATCATCCGGGTGCTTGGCCACTAAG 303

QY 233 LeuArgGluThrAsnAlaGlyArgCysAspThrArgGlnGlnTyrArgLysLeuLeuArg 252
Db 304 CTTGGGAGACCAATGCCGGCCGGTGTACACCAAGCAGCATACCGGAAGCTGCTCAGG 363

QY 253 SerThrLeuValLeuValProLeuPheGlyValHisTyrThrValPheMetAlaLeuPro 272
Db 364 TCCAGTTGGTGTGTGGCACTCTTCGGTGTCCACTACACCGTCTTCATGGCCCTTGGCG 423

QY 273 TyrThrGluValSerGlyThrLeuTyrGlnIleGlnMetHisTyrGluMetLeuPheAsn 292
Db 424 TACACCGAGGTCTCAGGACACTGTGGCAGATCCAGATGCATCATGATGATGCTCTTCAAC 483

QY 293 SerPheGlnGlyPhePheValAlaIleIleTyrCysPheCysAsnGlyGluValGlnAla 312
Db 484 TCCCTCCAGGATTTTGTGGCAATCAATATCTGTTCTGCAATGGTGGTGGTGGCGCA 543

QY 313 GluIleArgLysSerTyrSerArgTyrThrLeuAlaLeuAspPheLysArgLysAlaArg 332
Db 544 GAGATTAGGAAGTCTTGGAGCGGCTGGACACTGGCATTGGACTTCAAGCGTAAGACGCA 603

QY 333 SerGlySerSerSerTyrSerTyrGlyProMetValSerHisThrSerValThrAsnVal 352
Db 604 AGTGGAGTAGCAGCTACAGTATGGCCAAATGGTGTCCACCCAGAGTGTACCAATGTG 663

QY 353 GlyProArgAla---GlyLeuSerLeuProLeuSerProArg 365
Db 664 GGGCCCCCGTGCAGAAATCAGCCCTTCCCTCCCTTACCCCCCGC 705

RESULT 15
CB600301
LOCUS
DEFINITION AGENCOURT 17840463 NIH_MGC_238 Rattus norvegicus cDNA clone
IMAGE:7133139 5', mRNA sequence.
ACCESSION CK595861
VERSION CK595861
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 808)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLAM15036 row: 1 column: 01
High quality sequence stop: 641.
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1..808
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:7133139"
/tissue_type="testis, pooled"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_238"

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/notes="Organ: testis; Vector: pExpress-1; Site 1: EcoRV;  
Site 2: NotI; RNA obtained from testis tissue of 8 wk old  
animal. Tissues were snap-frozen and kept at -80C before  
RNA extraction and purification (Tri-reagent method). cDNA  
was primed using oligo-dT primer:  
5'-pgAGATTGATCGAGCGCCGCC(T)25-3' and cloned into  
the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb  
resulted in an average insert size of 1.9 kb. This primary  
library is normalized (non-normalized primary library is  
NIH MGC 237) and was constructed by Express Genomics  
(Frederick, MD) "

Job time : 4202 secs

## ORIGIN

## Alignment Scores:

Pred. No.:	4.54e-104	Length:	808
Score:	1181.50	Matches:	228
Percent Similarity:	97.02%	Conservative:	0
Best Local Similarity:	97.02%	Mismatches:	6
Query Match:	51.75%	Indels:	2
DB:	7	Gaps:	1

US-09-869-565-2 (1-435) x CK595861 (1-808)

QY	145	valgluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysLysTyr	164
Db	3	GTGGAGGGGCTGTACTTGCACAGCCTCATCTTCATGGCCTTTTCTCAGAGAGAGTAC	62
QY	165	LeuTyrGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTyrVal	184
Db	63	CTGTGGGGCTTCACCACTTTTGGCTGGGGTCTACCGGCTGTCTTCGTGGCTGTGGGTC	122
QY	185	GlyValArgAlaThrLeuAlaAsnThrGlyCysTyrAspLeuSerSerGlyHisLysLys	204
Db	123	GGTGTACAGACCAACCTTGGCCACACTGGGTGCTGGGATCTGAGCTCCGGGCACAGAG	182
QY	205	TyrIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn	224
Db	183	TGGATCATCCAGGTGCCCATCTGGCATCTGTTGTGCTCAACTTCATCTTTTATCAAC	242
QY	225	IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg	244
Db	243	ATCATCCGGGTGCTTGGCCATAGCTTCGGGAGACCAATCGGGCCGCTGTGACCCAGG	302
QY	245	GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis	264
Db	303	CAGCAGTACCGGAAGCTGCTCAGTCCAGGTGGTGTCTGTCGCGCTCTTTGGTGCCAC	362
QY	265	TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGln	284
Db	363	TACACCGTCTTCATGGCCTTGGCGTACCCGAGGTCTCAGGGACATTTGTGGCAGATCCAG	422
QY	285	MetHisTyrGlnMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys	304
Db	423	ATGCATTATGAGATGCTCTTCAACTCTTCCAGGGATTTTTTGTGCCATCATATACTGT	482
QY	305	PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTyrPheSerArgTyrThrLeuAla	324
Db	483	TTCTGCAATGGTGCAGGTGCAGGCAGAGATTAGGAGTCATGGAGCCGCTGGACACTGGCG	542
QY	325	LeuAspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal	344
Db	543	TTGGACTTCAAGCGCAAGACACAGTGGGAGTAGCAGCTACAGCTATGGCCCAATGGTG	602
QY	345	SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro	364
Db	603	TCTCACAGAGTGTGACCAATGTGGCCCCCTGCGAGACTCAGCCCTNCCCCCTCAGCCCC	662
QY	365	ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGly	379
Db	663	GCCTGC---CCTCTGCACCTACAATGNCACCTC-CAGCTGCCTGGC	703

Search completed: November 24, 2004, 04:31:56

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 24, 2004, 04:32:02 ; Search time 1290 Seconds  
(without alignments)  
1827.494 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSIALLCCPVLS.....EASGARPPPLQGWETVM 435

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3640242 seqs, 2709731945 residues

Total number of hits satisfying chosen parameters: 7280484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0  
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2195	96.1	2051	15	US-10-267-730-3	Sequence 3, Appli
2	2187	95.8	1776	9	US-09-943-446-3	Sequence 3, Appli
3	2187	95.8	2065	16	US-10-152-319A-1741	Sequence 1741, Ap
4	2146	94.0	1776	9	US-09-943-446-4	Sequence 4, Appli
5	2146	94.0	1776	9	US-09-943-446-5	Sequence 5, Appli
6	2008	88.0	1948	15	US-10-225-567A-228	Sequence 228, App
7	2008	88.0	1948	16	US-10-305-720-1253	Sequence 1253, Ap
8	2002	87.7	1782	10	US-09-826-509-562	Sequence 562, App
9	2002	87.7	2010	15	US-10-267-730-4	Sequence 4, Appli
10	1957	85.7	1788	9	US-09-943-446-2	Sequence 2, Appli
11	1957	85.7	2177	9	US-09-943-446-1	Sequence 1, Appli
12	1710	74.9	1863	15	US-10-267-730-2	Sequence 2, Appli
13	1704.5	74.7	2192	16	US-10-062-674-1564	Sequence 1564, Ap
14	1687	73.9	1862	15	US-10-267-730-1	Sequence 1, Appli
15	1465	64.2	1609	15	US-10-372-095-1	Sequence 1, Appli
16	1133	49.6	21704	15	US-10-017-161-709	Sequence 709, App
17	1133	49.6	21704	15	US-10-292-798-621	Sequence 621, App
18	1130	49.5	2152	15	US-10-372-095-3	Sequence 3, Appli
19	1097	48.1	681	16	US-10-332-859-229	Sequence 229, App
20	1050.5	46.0	1896	15	US-10-395-027-523	Sequence 523, App
21	1050.5	46.0	2641	15	US-10-325-567A-226	Sequence 226, App
22	1050.5	46.0	2641	15	US-10-395-027-525	Sequence 525, App
23	1050.5	46.0	2641	15	US-10-395-027-850	Sequence 850, App
24	1050.5	46.0	2641	16	US-10-305-720-1463	Sequence 1463, Ap
25	1050.5	46.0	2641	17	US-10-283-975A-70	Sequence 70, Appl
26	1044.5	45.8	1653	10	US-09-826-509-564	Sequence 564, App
27	1036	45.4	2003	9	US-09-996-569-1	Sequence 1, Appli
28	820	35.9	637	16	US-10-332-859-9	Sequence 9, Appli
29	790.5	34.6	2771	15	US-10-225-567A-468	Sequence 468, App
30	790.5	34.6	2867	14	US-10-116-802-155	Sequence 155, App
31	778	34.1	2684	17	US-10-283-975A-48	Sequence 48, Appl
32	778	34.1	2834	9	US-09-954-456-286	Sequence 286, App
33	778	34.1	2834	9	US-09-954-456-951	Sequence 951, App
34	778	34.1	2834	9	US-09-954-456-1603	Sequence 1603, Ap
35	778	34.1	2834	10	US-09-873-367C-311	Sequence 311, App
36	778	34.1	2834	15	US-10-295-027-874	Sequence 874, App
37	758.5	33.2	1374	10	US-09-826-509-578	Sequence 578, App
38	757.5	33.2	1796	16	US-10-152-319A-1884	Sequence 1884, Ap
39	753	33.0	1616	16	US-10-305-720-1451	Sequence 1451, Ap
40	752	32.9	1650	18	US-10-855-676-3	Sequence 3, Appli
41	752	32.9	1703	15	US-10-225-567A-309	Sequence 309, App
42	738	32.3	1323	10	US-09-826-509-566	Sequence 566, App
43	734.5	32.2	1280	16	US-10-051-874-9	Sequence 9, Appli
44	696	30.5	1640	15	US-10-325-567A-470	Sequence 470, App
45	689.5	30.2	1869	9	US-09-935-371-40	Sequence 40, Appli

# ALIGNMENTS

RESULT 1  
US-10-267-730-3  
; Sequence 3, Application US/10267730  
; Publication No. US20030153041A1  
; GENERAL INFORMATION:  
; APPLICANT: Segre, Gino V.  
; APPLICANT: Kronenberg, Henry M.  
; APPLICANT: Abou-Samra, Abdul-Badi  
; APPLICANT: Juppner, Harald  
; APPLICANT: Potts, Jr., John T.  
; APPLICANT: Schipani, Ernestina  
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME  
; FILE REFERENCE: 00786/071005  
; CURRENT APPLICATION NUMBER: US/10/267,730  
; CURRENT FILING DATE: 2003-01-27  
; PRIOR APPLICATION NUMBER: US 08/471,494  
; PRIOR FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2051





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US-10-152-319A-1741
; Sequence 1741, Application US/10152319A
; Publication No. US20040072160A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgins, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/10/152,319A
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1741
; LENGTH: 2065
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_020073
US-10-152-319A-1741

Alignment Scores:
Pred. No.: 3,39e-235 Length: 2065
Score: 2187.00 Matches: 434
Percent Similarity: 73.43% Conservative: 0
Best Local Similarity: 73.43% Mismatches: 1
Query Match: 95.80% Indels: 156
DB: 16 Gaps: 1

US-09-869-565-2 (1-435) x US-10-152-319A-1741 (1-2065)
QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuLeuLeuLeuSer 20
Db 73 ATGGGGGCGCGCGGATCGCACCAGCCCTGGCGCTCTTCTCTGCTGCGCCAGTGCAGC 132
QY 21 SerAlaTyAlaLeu----- 25
Db 133 TCGCATATGCGTGGTGGATGGGACGATGCTTTTACCAAGAGGAACAGATTTCCTG 192
QY 25 ----- 25
Db 193 CTGCACCGTCCCGAGCGCAATGTGAAAGCTCTCAAGGAAGTTCTGCACACAGCGCC 252
QY 25 ----- 25
Db 253 AACATAATGGAGTCAGACAGGGCTGGACACACAGCATCTACGTCAGGGAAGCCAGAAA 312
QY 25 ----- 25

313 GAGNAGGCATCGGGAAAGTTCTACCTGAGTCTAAAGAGAACAGGACGTGCCCCACCGGC 372
25 ----- 25
373 AGCAGGCGCAGAGGGCGTCCCTGTCTGCCGAGTGGGACAAATCGTTTGTGTGCCATT 432
25 ----- 25
433 GGGGCAACCGTGAAGTGGTGGCAGTACCTTGTCCGATTACATTTATGACTTCAATCAC 492
25 ----- 25
493 AAAGGCCATCGCTACAGACGCTGTGACCGCAATGGCAGCTGGGAGGTGGTTCCAGGGCAC 552
25 ----- 25
553 AACCGGACGTGGGCCAACTACAGCGAGTGCTCAAGTTCTATGACCAATGAGACGCGGAA 612
26 ---GluValPheAspArgLeuGlyMetIleTyThrValGlyTyThrSerMetSerLeuAla 44
613 CGGAGGTATTGACCGCTTAGCATATCTACACCGTGGGATACTCCATGTCTCTCGCC 672
45 SerLeuThrValAlaValLeuIleLeuAlaTyThrPheArgArgLeuHisCysThrArgAsn 64
673 TCCCTCAGCGTGGCTGTGCTCATCTGGCCTATTTAGCGCGCTGCACTGCACGCGCAAC 732
65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84
733 TACATCCACATGCACATGTTCTGTGCTTATGCTGCGCGCGCGAGCATCTTCGTGAAG 792
85 AspAlaValLeuTyThrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104
793 GACGCTGTGCTTACTCTGGCTTCACGCTGAGTGGAGCCGAGCGCTTCACAGAGAGAG 852
105 LeuHisIleIleAlaGlnValProProProAlaAlaAlaAlaValGlyTyThrAlaGly 124
853 TTGCACATCATCGCGCAGGTGCCACCTCCCGCGCGCTGCCGCGTAGCTAGCTAGCTGGC 912
125 CysArgValAlaValThrPhePheLeuTyThrPheLeuAlaThrAsnTyThrIleLeu 144
913 TGCCGCGTGGCGGTGACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 972
145 ValGluGlyLeuTyThrLeuHisSerLeuIlePheMetAlaPhePheSerGlyLysLeuTy 164
973 GTGGAGGGCTGACTTGACAGCCCTCATCTTCTGCGCTTCTTCTTCTTCTTCTTCTTCT 1032
165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184
1033 CTGTGGGGCTTCCACCATCTTGGCTGGGGTCTACCGGCTGTCTTCTGTGGCTGTGTGGTC 1092
185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLys 204
1093 GGTGTGAGAGCAACCTTGGCCAACTGGGTGTGGATCTGAGCTCCGGGCAACAAG 1152
205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224
1153 TGGATCATCAGGTGCCATCTCTGGCATCTGTGTCTCACTTCACTTCACTTCTTCTTCT 1212
225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244
1213 ATCATCCGGGTGCTTCCCACTTAAGCTTCGGAGACCAATGCGGGCGGTGTGACACAGG 1272
245 GlnGlnTyArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
1273 CAGCAGTACCGGAAGCTGCTCAGGTCCAGCTTGGTGTGCTGCTTCTTCTTCTTCTTCT 1332
265 TyrThrValPheMetAlaLeuProTyThrGluValSerGlyThrLeuTrpGlnIleGln 284
1333 TACACCGCTCTTCAATGGCTTGGCTACACGAGGTCTCAGGAGCATTTGGGAGATCCAG 1392
285 MetHisTyGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleLeuTyCys 304
1393 ATGCATTATGAGATGCTTCAACTCCTTCCAGGGATTTTGTGCTGCTTCTTCTTCTTCT 1452
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QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324  
DB 1453 TTCTGCAATGGTGGAGTGCAGCAGAGATTAGAAAGTCATGGAGCGCTGGACACTGGCG 1512  
QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerTrpSerTrpGlyProMetVal 344  
DB 1513 TTGGACTTCAGAGCGCAAGCAGCAAGTGGAGTAGCAGCTACGCTATGGCCCAATGGTG 1572  
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364  
DB 1573 TCTCACAGAGTGTGACCAATGTGGGCCCGCGTGCAGGACTCAGCCTCCCGCTCAGCCCG 1632  
QY 365 ArgLeuProProAlaThrTrpAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384  
DB 1633 CGCCTGCCTCCTGCCACTACCAATGCCACTCCAGCTGCCTGGCCATGCCAAGCCAGGG 1692  
QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspGly 404  
DB 1693 GCTCCAGCCACTGAGACTGAAACCTACAGTCACTATGGCGGTTCCGAGACGATGGA 1752  
QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArgPro 424  
DB 1753 TTCCTTAACGGCTCCTGCTCAGCGCTGGATGAGGAGGCTCGGGTCTGGCGCGCGCT 1812  
QY 425 ProLeuLeuGlnGluGlyTrpGluThrValMet 435  
DB 1813 CCATTGTTGCAGGAAGAATGGGAAACAGTCAATG 1845

## RESULT 4

US-09-943-446-4  
; Sequence 4, Application US/09943446  
; Patent No. US2002014677A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Castleberry, Tessa A.  
; APPLICANT: Lu, Bihong  
; APPLICANT: Owen, Thomas A.  
; APPLICANT: Smock, Steven L.  
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor  
; FILE REFERENCE: PC1089LAGPR  
; CURRENT APPLICATION NUMBER: US/09/943,446  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 60/229,170  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1776  
; TYPE: DNA  
; ORGANISM: Mus Musculus  
US-09-943-446-4

Alignment Scores:  
Pred. No.: 1,1e-230 Length: 1776  
Score: 2146.00 Matches: 426  
Percent Similarity: 72.42% Conservative: 2  
Best Local Similarity: 72.08% Mismatches: 7  
Query Match: 94.00% Indels: 156  
DB: 9 Gaps: 1

US-09-869-565-2 (1-435) x US-09-943-446-4 (1-1776)

QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuSer 20  
DB 1 ATGGGACCGCCGGATCGCACCAGCCTGGCGCTCCTTCTGCTGCCAGTGTCTCAGC 60  
QY 21 SerAlaThrAlaLeu----- 25  
DB 61 TCCGATATGCGCTGGTGGAGCAGCATGTCTTTACCAAGAGAACAGATTTCCTCTG 120  
QY 25 ----- 25

DB 121 CTGCACCGTGTCCAGCGCAATGTGCAAGCTGTCTCAAGAAAGTTCTGCACACAGCAGCC 180  
QY 25 ----- 25  
DB 181 AACATAATGGAGTCAGACAAAGGGTGGACTCCAGCATCTACGTACGGGAAGCCAGGA 240  
QY 25 ----- 25  
DB 241 GAGAAAGCACCGGAAAGTTCTACCCGAGTCTAAAGAGAAACAAGGATGTGCCACCGCC 300  
QY 25 ----- 25  
DB 301 AGCAGCGCCGAGGCGCTCCCTGTCTGCAGAGTGGGACACATCGTTTGTGTGGCCATTG 360  
QY 25 ----- 25  
DB 361 GGGGCACCAGGTGAAGTGTGGCAGTACCTTGTGCCGATTACATTATGACTTCAACCC 420  
QY 25 ----- 25  
DB 421 AAAGGCCATGCTACAGACGCTGCAGCCGAATGGCAGCTGGGAGGTGGTTCCAGGGC 480  
QY 25 ----- 25  
DB 481 AACCGCAGCTGGGCCAACTACAGCGAGTGCCTCAAGTTTCATGCCAATCAGACTCGG 540  
QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44  
DB 541 CGGAGGTATTGACCGCTGGCATGATCTACACCGTGGGATATTCCATGTCTCTTGC 600  
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64  
DB 601 TCCCTCACCGTGGCTGTCTCATCTAGCTATTTTAGCGCGCTGCATCTGCACGCGCA 660  
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84  
DB 661 TACATCCACATGCACATGTTCTGTCTGTTATGTCTGCGCGCGCGAGGATCTTCTG 720  
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104  
DB 721 GACGCTGTGCTCTACTCTGGCTTCACGCTGGATGAGCGCGAGCGCTCACGAGGAAG 780  
QY 105 LeuHisIleIleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGly 124  
DB 781 TTGCATATCATCGCGCAGGTGCGCTCCGCGCGCTGCGCGCTGGCTACGCTGCG 840  
QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTrpIleLeu 144  
DB 841 TGCCGTGTGGCGGTGACCTTCTTCTCTACTCTGCGCTACCACTACTCTGGATTCTG 900  
QY 145 ValGluGlyLeuTyrLeuHisSerIlePheMetAlaPhePheSerGluLysLysTyr 164  
DB 901 GTGGAGGAGTGTACTTACACAGCCTCATCTTCATGGCTTTTCTCAGAGAAGATAT 960  
QY 165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184  
DB 961 CTGTGGGCTTTCACCATCTTTGGCTGGGCTGCGCGCTGTCTTCTGCTGGCTGTG 1020  
QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLys 204  
DB 1021 GGTGTGAGAGCAACTTGGCCCAACACTGGGTGTGGGACCTGAGCTCTGGGCGCAAGAG 1080  
QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224  
DB 1081 TGGATCATCCAGTGCCCATCTTGGCATCTGTGTGTCTCACTTCACTTCTTTATCAAC 1140  
QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244  
DB 1141 ATCATCGGGTGTGTCACCTAAGCTTCGGGAGCAATGGCGCGCTGTGACACAGG 1200  
QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264  
DB 1201 CAGCAGTACCGGAAAGTGTCTCAGGTTCACAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1260





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QY 225 llelleArgValLeuAlaThrIysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244
DB 1141 ATCATCCGGGTCTTTGCCACTAAGCTTCGGGAGACCAATCGCGCGGTGTGACACCCAGG 1200
QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
DB 1201 CAGCAGTACCGAAGCTGCTCAGGTCACAGTTGGTGTCTTGTCCACTCTTCCTGGTGTCCAC 1260
QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284
DB 1261 TACACCGTCTTCATGGCCCTTGGCGTACACCGAGGTCTCAGGGACACTGTGGCAGATCCAG 1320
QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys 304
DB 1321 ATGCATATGAGATGCTCTTCAACTCCTTCCAGGATTTTGTGGCCATCATATACTGT 1380
QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324
DB 1381 TTCTGCATGTGTAGGTGAGCGACAGAGATTAGAAAGTCTTGGAGCGCTGGACACTGGCA 1440
QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344
DB 1441 TTGGACTTCAAGCGTAAAGCACGAAGTGGAGTAGCAGCTACAGCTATGGCCCAATGGGT 1500
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
DB 1501 GCACACAGAGGTGACCAATGTGGGCCCCCGTGCAGGACTCAGGCTTCCCTTAGCCCC 1560
QY 365 ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384
DB 1561 CGCTGTCTCTGCCACACCAATGGCCACTCCAGCTGCTGGCCAGCCCAAGCCGGGC 1620
QY 385 AlaProAlaThrGluThrGluThrProValThrMetAlaValProLysAspAspGly 404
DB 1621 GCTCCAGCCATTGAGAACGAACCATACCACTTACTATGACAGTTCCCAAGGACGACGGC 1680
QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProPro 424
DB 1681 TTCCTTAATGGCTCCTGTCTGGGTCTGGATGAGGAGGCTCTGGGTCTGCGCGGCACCT 1740
QY 425 ProLeuLeuGlnGluGlyTrpGluThrValMet 435
DB 1741 CCATGTGTCGAGGAAGAATGGGAACAGTCATG 1773
RESULT 6
US-10-225-567A-228
; Sequence 228, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-228
Alignment Scores:
Pred. No.: 4,27e-215 Length: 1948
Score: 2008.00 Matches: 399
Percent Similarity: 68.97% Conservative: 10
Best Local Similarity: 67.28% Mismatches: 26
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Query Match: 87.95% Indels: 158
DB: 15 Gaps: 3
US-09-869-565-2 (1-435) x US-10-225-567A-228 (1-1948)
QY 1 MetGlyAlaAlaAArgIleAlaProSerLeuAlaLeuLeuLeuCysCysProValLeuSer 20
DB 29 ATGGGGACCGCGCCGATCGACCCCGCTGGCGCTCTGCTCTGCTGCCCCGTGCTCAGC 88
QY 21 SerAlaTyrAlaLeu----- 25
DB 89 TCCGGGTACGGCTGTGGATGCAGATGACGTCACTAAAGAGAAACAGATCTTCTCTG 148
QY 25 ----- 25
DB 149 CTGCACCGTGTCTCAGGCCAGTGCAGAAAAACGGCTCAAGGAGGTCTCTGCAGAGCCAGCC 208
QY 25 ----- 25
DB 209 AGCATAAATGGAATCAGAACAGGATGAGACATCTGCGTCCACATCAGGGAAGCCAGGAAA 268
QY 25 ----- 25
DB 269 GATAAGGCATCTGGGAAGCTCTACCCCTGAGTCTGAGGAGGACAGAGAGCCACCTAGTGC 328
QY 25 ----- 25
DB 329 AGCAGGTACCGAGCGCGCCCTGTCTGCGGAAATGGGACCACATCCTGTGTGGCGGCTG 388
QY 25 ----- 25
DB 389 GGGGCACCAAGGTGAGTGGTGGCTGTGCCCTGTCCGAGTACATTTATGACTTCAATCAC 448
QY 25 ----- 25
DB 449 AAAGGCCATGCTACCGACGCTGTACCCGCAATGGCAGCTGGGAGCTGGTGCCTGGGCAC 508
QY 25 ----- 25
DB 509 AACAGGACGTGGGCAACTACAGCGAGTGTGTCAAAATTTCTCACCAATGAGACTCGTCAA 568
QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44
DB 569 CGGGAGGTGTTGACCGCTCGGCATGATTTACACCGCTGGGCTACTCGCTGTCTCCGTGGC 628
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64
DB 629 TCCCTCACCGTAGTGTGTCTCATCTGGCCTACTTTAGCGCGCTGCACTGCACGGCGCAAC 688
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIys 84
DB 689 TACATCCACATGCACCTGTTCTGTCTTCATGTGTGCGCGCTGAGCGCTCTTCGTCAAG 748
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104
DB 749 GACGTGTGCTCTACTCTGGCGCACCGCTTGATGAGGTGAGCGCTCACCGAGAGAGAG 808
QY 105 LeuHisIleIleAlaGlnValProProProAlaAlaAlaAlaValGlyTyrAlaGly 124
DB 809 CTGGCGGCATCGCCCGAGCGCCCCCGCGCTGCCACCGCGCTGCCGGGTACCGCGGC 868
QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144
DB 869 TGCAGGGTGGTGTGACCTTCTTCTTACTCTCTGGCCACCACTACTACTGTGATTCTG 928
QY 145 ValGluGlyLeuTyrLeuHisSerIleIlePheMetAlaPhePheSerGluLysIleTyr 164
DB 929 GTGAGGGGCTGTACCTGCACAGCCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 988
QY 165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184
DB 989 CTGTGGGGCTTCACAGTCTTCGGCTTGGGTCTGCGCGGTGTCTTCTTCTTCTTCTTCTTCT 1048
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QY	185	GlyValArgAlaThrLeuAlaAenThrGlyCysTrpAspLeuSerSerGlyHisLysLys	204
DB	1049	AGTGT CAGAGCTACCTGGCGCAACACGGGTGTGGACTTGAGCTCGGGAAACAAAAG	1108
QY	205	TrpIleIleGlnValProIleLeuAlaSerValValLeuAenPheIleLeuPheIleAsn	224
DB	1109	TGGATCATCCAGGTGCCATCCCTGGGCTCATTTGTCTCAACTTCATCTCTTCATCAAT	1168
QY	225	IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg	244
DB	1169	ATGTCGCGGTGTGCGCACCAAGCTCGGGAGACCAACGCGCGCGGTGTGACACACGG	1228
QY	245	GlnGlnTyrArgLysLeuLeuArgSerThrLeuValValLeuValProLeuPheGlyValHis	264
DB	1229	CAGCAGTACCGGAAGCTGCTCAAATCCACGCTGGTGTCTATGCCCTCTTTGGCGTCCAC	1288
QY	265	TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln	284
DB	1289	TACATTGCTTCATGGCCACACCATACACGAGGTCTCAGGGACGCTCTGGCAAGTCCAG	1348
QY	285	MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys	304
DB	1349	ATGCATATCAGATGCTCTTCACTCTTCAGGGATTTTTTGTGCGCAATCATATACTGT	1408
QY	305	PheCysAsnGlyGluValGlnAlaGluIleAArgLysSerTrpSerArgTrpThrLeuAla	324
DB	1409	TTCTGCAATGGCGAGGTACAAAGCTGAGATCAAGAAATCTTTGGAGCGCTGGACACTGGCA	1468
QY	325	LeuAspPheLysArgLysAlaArgSerGlySerSerSerTyrSerTyrGlyProMetVal	344
DB	1469	CTGACTTCAAGCGAAAGCAGCAGCGGAGCAGCAGCTATAGCTACGCCCCCATGGTG	1528
QY	345	SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro	364
DB	1529	TCCACACAAAGTGTGACCAATGTGCGCCCGCTGTGGACTCGGCCTGCCCTCAGCCCC	1588
QY	365	Arg---LeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysPro	383
DB	1589	CGCCTACTGCCCACTGCCACCAACCAACGGCCACCCTCAGCTGGCTGGCCATGCCAAGCCA	1648
QY	384	GlyAlaProAlaThrGluThr---GluThrLeuProValThrMetAlaValProLysAsp	402
DB	1649	GGAGACCCACCCCTGGAGACCCCTCGAGACACACACCCTCCCATGGCTGTCTCCCAAGGAC	1708
QY	403	AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArg	422
DB	1709	GATGGGTTCCTCAACGGCTCTGCTCAGGCTGTGACGAGAGGCTCTGGGCTGTAGCGG	1768
QY	423	ProProProLeuLeuGlnGluGlyTrpGluThrValMet	435
DB	1769	CCACCTGCCCTGTCTACAGGAAGAGTGGGACAGCTCATG	1807

RESULT 7

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RESULTS /
US-10-305-720-1253
; Sequence 1253, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; CURRENT APPLICATION NUMBER: 05/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1253
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g190721

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45 SerLeuThrValAlaValLeuLeuLeuAlaTyrPheArgArgLeuHisCysThrArgen 64  
628 TCCCTCACGTAAGCTGTGCTCATCTTGGCTACTTTAGCGGGCTGCACTGCACGGCAAC 687  
65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheVallys 84  
688 TACATCCACATGCACTGTCTCTGCTTTCATGCTGCGCGCTGAGCATCTTCGTCAAG 747  
85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104  
748 GACGCTGTGCTCTACTCTGGCGCCACGCTTGATGAGCTGAGCGCTCACCGGAGGAG 807  
105 LeuHisIleAlaGlnValProProProAlaAlaAlaAlaValGlyTyrAlaGly 124  
808 CTGCGCGCATCGCCACGCGCCCGCGCTGCCACCGCGCTGCCGCTGACGGCGC 867  
125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144  
868 TGCAGGGTGGCTGTGACCTTCTCTTACTTCTTCTGCGCCACCACTACTACTGGATTCTG 927  
145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysTyr 164  
928 GTGGAGGGGCTGTACCTGCACAGCCTCATCTTTCATGGCTTCTTCTCAGAGAAGTAC 987  
165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184  
988 CTGTGGGGCTTCACAGTCTTGGCTGGGGTCTGCCCGCTGTCTTCTGCTGTGGGTG 1047  
185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLys 204  
1048 AGTGTACAGAGTACCTGGCCAAACACCGGGTCTGGGACTTGGAGTCCGGGAACAAAG 1107  
205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224  
1108 TGGATCATCCAGGTGCCATCTGCGCTCCATGTGCTCAAGTTCATCTCTTCATCAAT 1167  
225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244  
1168 ATCGTCCGGGTGCTCGCCACCAAGCAGCGGGAGACCAACCGCGCGGTGTGACACAGG 1227  
245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264  
1228 CAGCAGTAGTCCGAAAGCTGTCAAAATCCACGCTGGTGTCTCATGCCCTCTTTGGCGTCCAC 1287  
265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284  
1288 TACATTGTCTTTCATGGCCACACCATACACCGAGGTCTCAGGGAGCGTCTGGCAAGTCCAG 1347  
285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPheValAlaIleIleTyrCys 304  
1348 ATGCACTATGAGTGTCTTCACTCTTCCAGGATTTTGTGCAATCATATACTGT 1407  
305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324  
1408 TTCTGCAATGCGAGGTCAAGCTGAGATCAAGAAATCTTGGAGCGCTGGACACTGGCA 1467  
325 LeuAspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344  
1468 CTGACTTTCAGCGAAAGGACGACGAGCGGGAGCAGCAGCTATAGCTACGGCCCCATGGTG 1527  
345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364  
1528 TCCACACAGTGTGACCAATGTGGCCCCCGTGTGGGACTCGGCTCGCCCCCTAGCCCC 1587  
365 Arg---LeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysPro 383  
1588 CGCCTACTGCCCACTGCCACCAACCAACGCCACCTCAGCTGCCTGGCCATGCCAAGCCA 1647  
384 GlyAlaProAlaThrGluThr---GluThrLeuProValThrMetAlaValProLysAsp 402  
1648 GGGACCCCGAGCCCTCGAGACCCCTCGAGACCAACACCTGCTGCTGCCAAGGAC 1707  
403 AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArg 422

Db 1708 GATGGGTTCCTCAACGGCTCTCGCTCAGCGCTGGACGAGGCGCTCTGGGCGCTGAGCG 1767  
QY 423 ProProProLeuLeuGlnGluGlyTrpGluThrValMet 435  
Db 1768 CCACCTGCGCTCTACAGGAGAGTGGGAGACAGTCATG 1806  
RESULT 10  
US-09-943-446-2  
; Sequence 2, Application US/09943446  
; Patent No. US20020146777A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Castleberry, Tessa A.  
; APPLICANT: Lu, Bihong  
; APPLICANT: Owen, Thomas A.  
; APPLICANT: Smock, Steven L.  
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor  
; FILE REFERENCE: PC10891AGR  
; CURRENT APPLICATION NUMBER: US/09/943,446  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 60/229,170  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1788  
; TYPE: DNA  
; ORGANISM: Canis Familiaris  
US-09-943-446-2  
Alignment Scores:  
Pred. No.: 2,04e-209 Length: 1788  
Score: 1957.00 Matches: 394  
Percent Similarity: 67.39% Conservative: 11  
Best Local Similarity: 65.56% Mismatches: 24  
Query Match: 85.72% Indels: 172  
DB: 9 Gaps: 5  
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QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuCysCysProValLeuSer 20  
Db 1 ATGGGGCGCGCTCCGAGATCGCGCGCTGCGCTGTGCTCTGTCTGCGCGGTGCTCAGC 60  
QY 21 SerAlaTyrAlaLeu----- 25  
Db 61 TCCGGTACGGCTGGTGGATGCAGATGCATGACCAAGAGGACAGATCTTCTCTG 120  
QY 25 ----- 25  
Db 121 CTGACCGCGCCAGCGCCAGTGGCCAGAAAGCGCTCAAGAAAGTCTCTGAGAGGCCAGCT 180  
QY 25 ----- 25  
Db 181 GACATATGGAATCAGACAAAGGATGGGCTTCTGATCCATCCATCAGGGAAGCTTAAGAA 240  
QY 25 ----- 25  
Db 241 GAGAAGGCATCTGGGAAGCTTACCTCAGTCCGAGGAGGACAAGAGGTGCCCACTGGC 300  
QY 25 ----- 25  
Db 301 AGCAGGACCGAGGGCGCCCTGCTGCGCGAGTGGGACACATCTTGTGGCGCGTGT 360  
QY 25 ----- 25  
Db 361 GGGGCAACAGGTGAGGTGGTGGTGTGCTGCTGCCGAGTGGGACACATCTTGTGGCGCGTGT 420  
QY 25 ----- 25  
Db 421 AAAGGCCATGCTACCTGCTGCTGTGACCGCAATGGCAGCTGGGAGCTGGTGGCTGGACAC 480



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QY 25 ----- 25
Db 686 AAGGCCATGCTACTACCGTTCGCTGTGACCGCAATGGCAGCTGGGAGCTGGTCCCTGGACAC 745
QY 25 ----- 25
Db 746 AACCGGAGCTGGGCCAACTACAGCGAGTGTGTCAAGTTCTTGACCAACGAGACTCGTGA 805
QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44
Db 806 CGGAGAGTGTTCACCGCTGGGCATGATCTACACCGTGGGCTACTCCGTGTGCTGGCC 865
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64
Db 866 TCCCTCACCGTGGCGTCTCATCTGCGCTTCTTTCAGGGCGCTGCACTGCACACGCAAC 925
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIys 84
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QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGlu 104
Db 986 GACCGGTGCTCTACTCGGGCGCCACGCTCCAGCGGCGGAGCGCTCCAGGAGAGAG 1045
QY 105 LeuHisIleIleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGly 124
Db 1046 CTGCGCGCATCGCGCAGCACCCCGCGCGCCACCGCGCGCGCC---GGCTACGCGCGC 1102
QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144
Db 1103 TGCAGGTAGTGTGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1162
QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluIlysiysTyr 164
Db 1163 GTGAGGGGCTGTACTGCTCATGCTCATGCTCATGCTCTCTCTCTCTCTCTCTCTCTCT 1222
QY 165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184
Db 1223 CTGTGGGGCTTCACGGTCTTCGGCTGGGGTCTGCGCGCGCTCTCTCTCTCTCTCTCTCT 1282
QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisIysIys 204
Db 1283 AGCGTGAGAGCCACCTCGGCCAACACCGGGTCTGGGACTTGAGCTCCGGGAACAGGAAG 1342
QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224
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QY 225 IleIleArgValLeuAlaThrIysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244
Db 1403 ATCGTCCGGGTCTCGCCACCAAGCTGGGAGACCAATGCGCGCGGTGTGACACGCGG 1462
QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264
Db 1463 CAGCAGTACCGGAAGCTCTCAAATCCACACTGGTGTGCTCATGCGCGCTCTTTGGCGTCCAC 1522
QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284
Db 1523 TACATCGTCTTCATGGCCACCGCTGACCGAGGTCTCAGGAGCGCTCTGGCAAGCTCCAG 1582
QY 285 MethIstYrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys 304
Db 1583 ATGCACACTACGAGATGCTCTCAACTCTCTCCAGGGATTTTGTGCGCATCATATACTGT 1642
QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324
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QY 325 LeuAspPheIysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344
Db 1703 CTGACTTCAAGCGCAAGGCCCGAAGTGGGAGCAGGTTACAGCTACGGCCCGATGGTG 1762
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364
Db 1763 TCTCACACGAGCGTGACCAAGTAGGCGCCCGCGGGAGCTTGGCTTGCCTCAGCCCC 1822
QY 365 ArgLeuProPro-----AlaThrThrAsnGlyHisSerGlnLeu 377
Db 1823 CGCTGTGCTCGCGCGCTGCGCCACACCGCCACCAACCAAGCGCCACCCCGCGATC 1882
QY 378 ProGlyHisAlaLysProGlyValAlaProAlaThrGluThrGluThrLeuProValThr 396
Db 1883 CCGGGCCACACCAAGCCAGGGGCGCGCG-----ACCTCCCGGCCACACCA 1927
QY 397 -----MetAlaValProLysAspGlyPheLeuAsnGlySerCysSerGlyLeuAsp 414
Db 1928 CTTGCCACGGCTGCTCCCAAGGACGATGGGTTCCTCAACGCTCTCTGCTCGGGGCTGGAC 1987
QY 415 GluGluAlaSerGlySerAlaArgProProProLeuLeuGlnGlyTyrGluThrVal 434
Db 1988 GAGGAGGCTTCGCGCGCGGAGCGGCGCTCCCGCCCTGCTGTCAGGAGGAGTGGGAGCGGTC 2047
QY 435 Met 435
Db 2048 ATG 2050

RESULT 12
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; Sequence 2, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267.730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Didelphoidea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (98) ... (1852)
US-10-267-730-2

Alignment Scores:
Pred. No.: 1.35e-181 Length: 1863
Score: 1710.00 Matches: 353
Percent Similarity: 64.25% Conservative: 28
Best Local Similarity: 59.53% Mismatches: 46
Query Match: 74.90% Indels: 166
DB: 15 Gaps: 8

US-09-869-565-2 (1-435) x US-10-267-730-2 (1-1863)
QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuCysCysProValLeuSer 20
Db 98 ATGGAGGGCGCCCGGATCTCCACAGGCTTGCCTTGTCTCTCTCTCTCTCTCTCTCTCTCT 157
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QY 21 SerAlaTyrAlaLeu----- 25  
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 QY 25 ----- 25  
 DB 218 CTGGCAATGCCAGGCCAGCTGTGACGAGCGCTGAAAGAGGTCTCAGGCGCTCGTAA 277  
 QY 25 ----- 25  
 DB 278 CTTGCTGAATCTGCCAAGACTGGATGTCAGGTCTGCAAGAGCAAAAGAGGAGAAACCT 337  
 QY 25 ----- 25  
 DB 338 GCAGAAAGCTTTATCCCCAGGAGGAGTCCAGGGAAGTTTCTGACAGGAGCGCGCTG 397  
 QY 25 ----- 25  
 DB 398 CAGGATGGCTTCTGCTTACCTGAGTGGGCAACAATTGTGTGCTGGCTGCTGGAGTGCC 457  
 QY 25 ----- 25  
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 QY 25 ----- 25  
 DB 518 GCCTATCGGCGTGTGACAGCAATGGCAGCTGGGAGCTGGTGGCTGGGAACAACCGACA 577  
 QY 26 -----GluVal 27  
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 QY 48 ValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyrIleHis 67  
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 QY 88 LeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeuHisIle 107  
 DB 818 CTCTACTCGGGGTTTCCACAGATGAATCGCGCATCACCGGAGGAGGAGCTGAGGGCC 877  
 QY 108 IleAlaGlnValProProAlaAlaAlaValGlyTyrAlaGlyCysArgVal 127  
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 QY 288 GluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleTyrCysPheCysAsn 307  
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 ; Sequence 1564, Application US/10062674  
 ; Publication No. US2004000559A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.  
 ; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS  
 ; FILE REFERENCE: PA-0026-1 CIP  
 ; CURRENT APPLICATION NUMBER: US/10/062,674  
 ; CURRENT FILING DATE: 2002-01-30  
 ; PRIOR APPLICATION NUMBER: US 09/625,102  
 ; PRIOR FILING DATE: 2000-07-24  
 ; NUMBER OF SEQ ID NOS: 2217  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 1564  
 ; LENGTH: 2192  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US2004000559A1 137252.5  
 ; NAME/KEY: unsure  
 ; LOCATION: (1) ... (2192)  
 ; OTHER INFORMATION: a, t, c, g, or other  
 US-10-062-674-1564  
 Alignment Scores: 7.22e-181 Length: 2192  
 Fred. No.: 1704.50 Matches: 393  
 Score:







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; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1r and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: Danio rerio
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1608)
US-10-372-095-1

Alignment Scores:
Pred. No.: 3,93e-154 Length: 1609
Score: 1465.00 Matches: 284
Percent Similarity: 79.66% Conservative: 45
Best Local Similarity: 68.77% Mismatches: 66
Query Match: 64.17% Indels: 18
DB: 15 Gaps: 4

US-09-869-565-2 (1-435) x US-10-372-095-1 (1-1609)

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Qy 46 LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
Db 475 CTTATGGTGGCCACAGTCATCTCTGGATACCTTCGACGGCTCCACTGCACCGAATCAC 534
Qy 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIleAsp 85
Db 535 ATCCACATGCACCTGTCTTCTATCGTTTCATGTGTGAGGCGCATTAGTATCTTCGTGAAGGAT 594
Qy 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
Db 595 GTGGTGCTGTACTCTGTGTCGGCGCTGCAGGAATGGAAACGAATCACTGTGAGGATCTC 654
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Db 655 AAATCCCATCACTGAAGCCCTCCT-----GCCAACAAAAACCCAGTTTATCGGCTGT 705
Qy 126 ArgValAlaValThrPheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeuVal 145
Db 706 AAGGTGGCGGTGAGCTCTTCTGTACTCTTGGCCACTAATTATTACTGGATTCGTGGT 765
Qy 146 GluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysLysTyrLeu 165
Db 766 GAAGGCGCTGTACCTGCACAGCTTATCTTCATGACCTTCTCTCAGACAGGAGTACCTC 825
Qy 166 TrpGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTrpValGly 185
Db 826 TGGGGCTTCACTCTCATTTGGTTGGGGTGTTCCTGCGATGTTTGTCAACCTCTGGGCGAGT 885
Qy 186 ValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTrp 205
Db 886 GTTAGAGCCACACTTGTGACACTGAGTGTGGGATTTGAGTGCAGGAACCTGAAATGG 945
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; 226 IleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGln 245
; 1006 ATTCGAGTCTTGGCAACAAACTTCGAGAAACAAATCGGGCAGATGTGACCCAGACAA 1065
; 246 GlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyr 265
; 1066 CAATATAGGAAGCTGTGAGTCACTCTGTCTCTCATGCGCTGTTCGGTTCCTACTAC 1125
; 266 ThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGlnMet 285
; 1126 ATAGTCTTCATGGCGATGCCTTACACAGAAAGTTTCGAGTACTGTGGCAATCCAGATG 1185
; 286 HisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCysPhe 305
; 1186 CATATGAATGCTCTTTAACTCAGTCCAGGATTTCTTTGTTCGATTATATATTGCTTC 1245
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; 1246 TGCACCGGAGGTCCAAAGCGGAATCAAGAGGCGCTGGAACAGAGGACTCTTGCTCTG 1305
; 326 AspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetValSer 345
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; 346 HisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerProArg 365
; 1366 CACACCAAGTGTACCAATGTGACCGCGGGGGCGCTGGCCCTTCACTCACCACCGA 1425
; 366 LeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGlyAla 385
; 1426 CTGGGGCAGCTCACCACTAACCGGCCACAGAAACCTTCGGGATACATAAAAAACGGCTCC 1485
; 386 ProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspGlyPhe 405
; 1486 GTTTCAGAAAAAC-----TCCATCCGCTCCTCGGTCACGAG 1521
; 406 LeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProProPro 425
; 1522 CTTCACTTTCAG-----GAGGAAGAGCTTCGAAAGACCTCCAGATCGAGAAA 1569
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Job time : 1309 secs
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 24, 2004, 03:09:56 ; Search time 117 Seconds  
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2642.677 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGARIAPSLALLCCPVLS.....EASGSARPPPLQEGWETVM 435

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/US09869565/runat 23112004 162646 29473/app query.fasta\_1.583  
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
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-NO\_MWAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPLBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2195	96.1	2051	1	US-07-864-475A-3
2	2195	96.1	2051	2	US-08-468-249A-3
3	2008	88.0	1948	4	US-09-016-434-1253
4	2002	87.7	2010	1	US-07-864-475A-4
5	2002	87.7	2010	2	US-08-468-249A-4
6	1710	74.9	1863	1	US-07-864-475A-2
7	1710	74.9	1863	2	US-08-468-249A-2
8	1687	73.9	1862	1	US-07-864-475A-1
9	1687	73.9	1862	2	US-08-468-249A-1
10	1465	64.2	1609	4	US-09-449-632-1
11	1130	49.5	2152	4	US-09-449-632-3
12	1050.5	46.0	2641	4	US-09-016-434-1463

13	1036	45.4	2003	3	US-08-468-011A-1	Sequence 1, Appli
14	1036	45.4	2003	3	US-09-236-468A-1	Sequence 1, Appli
15	1036	45.4	2003	5	PCT-US95-07085-1	Sequence 1, Appli
16	770	33.7	1377	1	US-08-112-817C-1	Sequence 1, Appli
17	753	33.0	1616	4	US-09-016-434-1451	Sequence 1451, Ap
18	696	30.5	1640	4	US-09-708-392-20	Sequence 20, Appli
19	696	30.5	1817	2	US-08-538-816A-3	Sequence 3, Appli
20	696	30.5	1817	2	US-09-076-651-3	Sequence 3, Appli
21	696	30.5	1817	3	US-09-208-394-3	Sequence 3, Appli
22	696	30.5	1844	2	US-08-538-816A-10	Sequence 10, Appli
23	696	30.5	1844	2	US-09-076-651-10	Sequence 10, Appli
24	696	30.5	1844	3	US-09-208-394-10	Sequence 10, Appli
25	696	30.5	1894	2	US-08-538-816A-8	Sequence 8, Appli
26	696	30.5	1894	2	US-09-076-651-8	Sequence 8, Appli
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30	689.5	30.2	1869	3	US-09-201-474-40	Sequence 40, Appli
31	687.5	30.1	2730	2	US-08-811-897A-39	Sequence 39, Appli
32	687.5	30.1	2730	2	US-08-855-213-39	Sequence 39, Appli
33	687.5	30.1	2730	3	US-09-201-474-39	Sequence 39, Appli
34	687	30.1	1664	4	US-09-016-434-1384	Sequence 1384, Ap
35	686	30.0	1575	2	US-08-811-897A-34	Sequence 34, Appli
36	686	30.0	1575	2	US-08-855-213-34	Sequence 34, Appli
37	686	30.0	1575	3	US-09-201-474-34	Sequence 34, Appli
38	686	30.0	1664	2	US-08-811-897A-42	Sequence 42, Appli
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40	686	30.0	1664	3	US-09-201-474-42	Sequence 42, Appli
41	685.5	30.0	1401	2	US-08-811-897A-32	Sequence 32, Appli
42	685.5	30.0	1401	2	US-08-855-213-32	Sequence 32, Appli
43	685.5	30.0	1401	3	US-09-201-474-32	Sequence 32, Appli
44	679	29.7	1455	2	US-08-811-897A-31	Sequence 31, Appli
45	679	29.7	1455	2	US-08-855-213-31	Sequence 31, Appli

#### ALIGNMENTS

#### RESULT 1

US-07-864-475A-3  
; Sequence 3, Application US/07864475A  
; Patent No. 5494806  
; GENERAL INFORMATION:  
; APPLICANT: Segre, Gino V.  
; APPLICANT: Kronenberg, Henry M.  
; APPLICANT: Abou-Samra, Abdul-Badi  
; APPLICANT: Juppner, Harald  
; APPLICANT: Potts, John T. [Jr.]  
; APPLICANT: Schipani, Ernestina  
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR  
; TITLE OF INVENTION: AND DNA ENCODING SAME  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/864.475A  
; FILING DATE: 04-06-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/681.702  
; FILING DATE: 05-04-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul T. Clark  
; REGISTRATION NUMBER: 30,162





1393	Db	ANGCATTATGAGATGCTCTTCAACTCCTCCAGGGATTTTTTGTGGCATCATATACTGT	1452
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1453	Db	TTCTGCAATGCTGAGGTGCAGGCAGAGATTAGGAGTTCATGGAGCCGCTGGACACTGGCG	1512
325	Qy	LeuAspPheLysArgLysAlaArgSerGlySerSerSerTyrSerTyrGlyProMetVal	344
1513	Db	TTTGGACTTCAAGCGCAAGCACGAAGTGGGAGTAGCAGCTACAGCTATGCGCCCAATGGTG	1572
345	Qy	SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro	364
1573	Db	TCTCACACAGAGTGTGACCAATGTGGGCCCCCGGTGCAGACTCAGCTTCCGCTTCAGCCCC	1632
365	Qy	ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly	384
1633	Db	CGCCTGCCTCTGCCACTACCAATGGCCACTCCAGCTGCCTGGCCATGCCAAGCCAGGG	1692
385	Qy	AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspAsnGly	404
1693	Db	GCTCCAGCCACTGAGACTGAAACCCCTACCACTCACTATGGCGGTTCCTCAAGGACGATGGA	1752
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1753	Db	TTCTTAAACGGCTCCTGCTCAGGCCTGGATGAGAGGCCCTCCGGGTCTGGCGGCCGCT	1812
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### RESULT 3

US-09-016-434-1253  
Sequence 1253, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HERewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1253:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1948 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear









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; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/864.475A
; FILING DATE: 04-06-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/681,702
; FILING DATE: 05-04-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/071002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1863
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-07-864-475A-2

Alignment Scores:
Pred. No.: 4,57e-173 Length: 1863
Score: 1710.00 Matches: 353
Percent Similarity: 64.25% Conservative: 28
Best Local Similarity: 59.53% Mismatches: 46
Query Match: 74.90% Indels: 166
DB: 1 Gaps: 8

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[illegible]

## RESULT 7

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US-08-468-249A-2
; Sequence 2, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1863 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 98..1853
US-08-468-249A-2

Alignment Scores:
Pred. No.: 4,57e-173 Length: 1863
Score: 1710.00 Matches: 353
Percent Similarity: 64.25% Conservative: 28
Best Local Similarity: 59.53% Mismatches: 46
Query Match: 74.90% Indels: 166
DB: 2 Gaps: 8

US-09-869-565-2 (1-435) x US-08-468-249A-2 (1-1863)

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QY 248 ArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyrThrVal 267  
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QY 308 GlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAlaLeuAspPhe 327  
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QY 328 LysArgLysAlaArgSerGlySerSerSerTyrSerTyrGlyProMetValSerHisThr 347  
Db 1529 AAGCGGAAGGCCGCGAGTGGCAGCAGTACCTACAGCTATGCGCCCATGGTGTACATACA 1588  
QY 348 SerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerProArgLeuPro 367  
Db 1589 AGTGTCACCAATGTGGGACCTCGAGG-GGGCTGGCCCTTGTCCCTCAGCCCTCGACTAGCT 1647  
QY 368 Pro-----AlaThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384  
Db 1648 CCTGGGCTGAGGCGAGTGCACATGGCCATCCAGTTGCTGCTGCTGCTGCTGCTGCTGCTG 1707  
QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValPro-----LysAsp 402  
Db 1708 -----TCCATTTCTGAGAACTCATCTGCTTTCATCTGCGCCCGAGAGCTGCGCAAGAT 1761

QY 403 AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArg 422  
Db 1762 GACGGGTATCTCAATGGC-----TCTGGACTTTATGAGCAATGTTTGGGAA---CAG 1812  
QY 423 ProProProLeuLeuGlnGluGlyTrpGluThrValMet 435  
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RESULT 9  
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; Sequence 1, Application US/08468249A  
; Patent No. 5866148  
; GENERAL INFORMATION:  
; APPLICANT: Segre et al., Gino V.  
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA  
; TITLE OF INVENTION: ENCODING SAME  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/468,249A  
; APPLICATION NUMBER: US/08/468,249A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/864,475  
; FILING DATE: 06-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/681,702  
; FILING DATE: 04-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00786/071003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1862 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 98..1643  
US-08-468-249A-1  
Alignment Scores:  
Pred. No.: 1,33e-170 Length: 1862  
Score: 1687.00 Matches: 353  
Percent Similarity: 64.25% Conservative: 28  
Best Local Similarity: 59.53% Mismatches: 46  
Query Match: 73.89% Indels: 167  
DB: 2 Gaps: 8  
US-09-869-565-2 (1-435) x US-08-468-249A-1 (1-1862)  
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QY 21 SerAlaTyrAlaLeu----- 25

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QY 25 ----- 25
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QY 25 ----- 25
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Db 578 TGGGCGAATTACAGCGAATGTGTCAAGTTTCTGACCAACGAGACCGGGAAACGGGAGTC 637
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QY 208 GlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIleArg 227
Db 1169 CAGGTGCCATCTCTGGCAGCTATTGTGTGAACCTTTATCTTTTATCAATAATCAGA 1228
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## RESULT 10

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US-09-449-632-1
; Sequence 1, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1609
; TYPE: DNA
; ORGANISM: zebrafish
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1608)
US-09-449-632-1

Alignment Scores:
Pred. No.: 6,51e-147 Length: 1609
Score: 1465.00 Matches: 284
Percent Similarity: 79.66% Conservative: 65
Best Local Similarity: 68.77% Mismatches: 66
Query Match: 64.17% Indels: 18
DB: 4 Caps: 4
```



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US-09-869-565-2 (1-435) x US-09-449-632-1 (1-1609)
QY 26 GluValPheAspArgLeuGlyMetIleThrValGlyTyrSerMetSerLeuAlaSer 45
DB 415 GAGGTTTTCGACAGACTTACCTGATCTACACAGTGGGCTACTCCATCTCTCGGATCA 474
QY 46 LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
DB 475 CTTATGTTGGGACACAGTCTCTCGGATCTTTCACGGCTCCACTGCACGAGAACTAC 534
QY 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAsp 85
DB 535 ATCCACATGCACCTGTTTCTATCGTTTCATGTTGAGGGCCATTAGTATCTTCTGAGGAT 594
QY 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
DB 595 GTGGTGTCTGTACTCTGTGTTGGCGCTGCAGGAAATGGAACGAATCACTGTGGAGATCTC 654
QY 106 HisIleIleAlaGlnValProProAlaAlaAlaAlaValGlyTyrAlaGlyCys 125
DB 655 AAATCCATCACTGAAGCCCTCTCT-----GCCAAACAAACCCAGTTTATCGGCTGT 705
QY 126 ArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTyrIleLeuVal 145
DB 706 AAGGTGGCGGTGACGCTCTCTGTACTCTTGGCCACTAATTATTACTGGATTCTGGTG 765
QY 146 GluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluIleLysTyrLeu 165
DB 766 GAAGGCTGTACCTGCACAGCTTATCTTCATGACCTTCTCTCAGACGGAAGTACCTC 825
QY 166 TrpGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTyrValGly 185
DB 826 TGGGGCTTCACCTGATGGTGGTGGTGGTCTCGATGTTTGTCCACCATCTCGGCGAGT 885
QY 186 ValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLysTyr 205
DB 886 GTTAGGCCACACTGTGCTGACACTGAGTCTGGGATTGAGTGCAGGAACTGAAATGG 945
QY 206 IleIleGlnValProIleLeuAlaSerValValLeuAsnPhelleLeuPheIleAsnIle 225
DB 946 ATTGTGACAGATCCCATCTTACTGCAATGTTGTCAATTTTGTGTTCTCTGAATATA 1005
QY 226 IleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGln 245
DB 1006 ATTCGAGTCTTGGCAACAAACTTCGAGAAACAAATGGCGGACATGACACACAGAA 1065
QY 246 GlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyr 265
DB 1066 CAATATAGGAAGCTGCTGAAGTGCAGCTCTGTCTCATGCGCTTGTCTGCTGTTCACTAC 1125
QY 266 ThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGlnMet 285
DB 1126 ATAGTCTTTCATGGCGATGCGCTTACACAGAAGTTTCTGGAGTACTGTGGCAATCCAGATG 1185
QY 286 HisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCysPhe 305
DB 1186 CATATGAAATGCTCTTAACTCAGTCCAGGATCTTGTGTGGATTATATATGTCTTC 1245
QY 306 CysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTyrThrLeuAlaLeu 325
DB 1246 TGCAACGAGAGGTTCCAAAGCGAAATCAAGAAGCCCTGGAACAGAGGACTCTTGTCTG 1305
QY 326 AspPheLysArgLysAlaAspSerGlySerSerSerTyrSerTyrGlyProMetValSer 345
DB 1306 GACTTCAAGAGAAAAAGCCAGGAGCGGAGTAAACACATACATGATGAGCCCATGTTTCT 1365
QY 346 HisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerProArg 365
DB 1366 CACACCACTGTATCAATGTCAACGCGCGGCGGCGCTGCGGCTTCACTCACCACCAACCGA 1425
QY 366 LeuProProAlaThrThrAsnGlnHisSerGlnLeuProGlyHisAlaLysProGlyAla 385
DB 1426 CTGGGGCAGCTCACCACCTAAAGGCCACAGAAACCTTCGGGATATACATAAAAAACGGCTCC 1485
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386 ProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspGlyPhe 405
DB 1486 GTTTCAGAAAAC-----TCCATCCGCTCCTCGGGTCACGAG 1521
QY 406 LeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProPro 425
DB 1522 CTTCACTTCAG-----GAGGAAGAGCGCTTCAAGACCTTCCAGATGGAGAAA 1569
QY 426 LeuLeuGln-----GluGlyTyrGluThrValMet 435
DB 1570 ACCATCCAGGTGGTGGAGGAGGAAGAGAACCGTCATG 1608
RESULT 11
US-09-449-632-3
; Sequence 3, Application US/09449632
; Patent No. 6541220
; GENERAL INFORMATION:
; APPLICANT: Jpner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740001/SRL/M-G
; CURRENT APPLICATION NUMBER: US/09/449,632
; CURRENT FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2152
; TYPE: DNA
; ORGANISM: zebrafish
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (394)..(2019)
; NAME/KEY: misc feature
; LOCATION: (2125)..(2125)
; OTHER INFORMATION: n is any nucleotide of a,t,g or c
US-09-449-632-3
Alignment Scores:
Pred. No.: 8,38e-111 Length: 2152
Score: 1130.00 Matches: 230
Percent Similarity: 72.09% Conservatives: 49
Best Local Similarity: 59.43% Mismatches: 74
Query Match: 49.50% Indels: 34
DB: 4 Gaps: 7
US-09-869-565-2 (1-435) x US-09-449-632-3 (1-2152)
QY 26 GluValPheAspArgLeuGlyMetIleThrValGlyTyrSerMetSerLeuAlaSer 45
DB 799 GAAGTGTTCGAGCGCTTACCTCATGTACACTATTGGATCTCCATATCACTGCGACGG 858
QY 46 LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
DB 859 TTACTGTGGCGGTCTCTATCTTGTCTATTTCAACGCTCTCCACTGCACCTGTAACCTAC 918
QY 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAsp 85
DB 919 ATCCACATCCACCTTTCACCTCGTTTCATATGTCAGCAATCAGTATTTTGTGAAAGAC 978
QY 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
DB 979 GCGCTTCTTTCAGCGCGTCACGAATGAGAGAACTAGAGAGTGGCGAGTGGCAACAAAGA 1038
QY 106 HisIleIleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGlyCys 125
DB 1039 CCCATGGT-----GGCTGC 1053
QY 126 ArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTyrIleLeuVal 145
DB 1054 AAGCTCTGTGAGCCCTTCTTCTGTATCTGTGTCGACCAATCAATATTATGGATCCTGTG 1113
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QY 146 GluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPheSerGluLysLysTyrLeu 165
Db 1114 GAGGGTTGTACTGTGATAGTCTGATCTTCATGGCCTTCTGTCTGATAAGAACTGCCTG 1173
QY 166 TrpGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTyrValGly 185
Db 1174 TGGGCTTGACATCATAGCTGGGGATCCAGCAGTGTGTGTCTATATGGTCACT 1233
QY 186 ValArgAlaThrLeuAlaAsnThrGlyCysTyrAspLeuSerSerGlyHisLysTyr 205
Db 1234 GCCAGGGTGTCTCTGGCAGACACAGCTGGGATATCATGTCAGTCAGCAATTTGAAATGG 1293
QY 206 IleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsnIle 225
Db 1294 ATTATCAAGTACCAATCTGGCAGCATTGTGTAACTCTTCCTCTCCCAATATC 1353
QY 226 IleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArgGln 245
Db 1354 ATCAGGGTTTGGCCTTAAGTTGTGGAAACAAACACGGGAACTGGACCTAGACAG 1413
QY 246 GlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHisTyr 265
Db 1414 CAGTACAGGAAGCTGCTGAAGTCAACAAATGCTGTATGCCACTGTTTGGAGTTCATTAC 1473
QY 266 ThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGlnMet 285
Db 1474 ATGCTGTTCATGCTCTTCGTCACATGATGTGACTGTTGTGTGAGCAGATTCGTATG 1533
QY 286 HisTyrGluMetLeuPheAsnSerPheGlnGlyPheValAlaIleIleTyrCysPhe 305
Db 1534 CATTACGAGATGCTCTTCAATCTTCACAGGGTTTCTTTGTGGGTTTATTACTGCTTC 1593
QY 306 CysAsnGlyGluValGlnAlaGluIleArgLysSerTyrSerArgTyrThrLeuAlaLeu 325
Db 1594 TGAATGGGAGGTGAGGAGCAGAGGTGAAGAAGCCTGTTGTGACGACAGTCTTGGCTTA 1653
QY 326 AspPheLysArgLysAlaArg-----SerGlySerSerSerTyrSerTyrGly 341
Db 1654 GACTGAAGCAGAGAGCTCAAGTCCACAGAGTGGCGGATGTGAAGTGTGTACTATGGA 1713
QY 342 ProMetValSerHisThrSerValThrAsnVal-----GlyProArgAla 356
Db 1714 GGAATGATGCCACACACACAGAGCGTGTCTTAGTGTGAGTGTGCTGCTAAAGGC 1773
QY 357 GlyLeuSerLeuProLeuSerProArgLeuProProAlaThrThrAsnGlyHisSerGln 376
Db 1774 GGTCTTCTCTG-----CACACCATAGGAGCCAAAGACAAATCCCATCTACAA 1821
QY 377 LeuProGlyHisAlaLysProGlyAlaProAlaThrGluThrGluThrLeu-----Pro 394
Db 1822 CATTGAGAACTTA-----CCGCGTACGCGCTCAGGACACAGAGACTTTGTATTACCCA 1878
QY 395 ValThrMetAlaValProLys 401
Db 1879 GTG-----GTCCCAAAG 1890

```

## RESULT 12

```

US-09-016-434-1463
; Sequence 1463, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA

```

```

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1463:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2641 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G887966
; US-09-016-434-1463

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## Alignment Scores:

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Pred. No.: 3,88e-102 Length: 2641
Score: 1050.50 Matches: 208
Percent Similarity: 68.91% Conservative: 58
Best Local Similarity: 53.89% Mismatches: 85
Query Match: 46.01% Indels: 35
DB: 4 Gaps: 7

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US-09-869-565-2 (1-435) x US-09-016-434-1463 (1-2641)

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QY 26 GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSer 45
Db 557 GAATCTCTTGAACGCTCTATGTATATGATATACCTGGCTACTCCATCTCTTTGGTTCC 616
QY 46 LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
Db 617 TTGGCTGTGGCTATTCTCATCTATGGTTACTTTCAGACGATTGCTAGGAACTAT 676
QY 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLysAsp 85
Db 677 ATCCATGACACTATTGTGTCTTTCATGCTGAGAGCTACAAGCATCTTTGTCAAGAC 736
QY 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
Db 737 AGAGTAGTCCATGCTCATAGGAGTAAAGAGCTGGAGTCCCTA----- 781
QY 106 HisIleIleAlaGlnValProProProAlaAlaAlaValGly----- 121
Db 782 -----ATAATGACGAGTATGACCAAAATTCATTGAGGCAACTCTCTGGGACAAATCA 835
QY 122 ---TyrAlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyr 140
Db 836 CAATATATCCGGTGCAGAGTGTGTGTGATGTTATTACTTCTCTGGCTACAAATAT 895
QY 141 TyrTrpIleLeuValGluGlyLeuTyrLeuHisSerIlePheMetAlaPheSer 160
Db 896 TATTGGATCCTGTGGAAAGTCTTACCTGCATAATCTCATCTTTGGGCTTCTTTTCG 955
QY 161 GluLysLysTyrLeuTyrGlyPheThrIlePheGlyLeuProAlaValPheVal 180
Db 956 GACACCAATACCTGTGGGCTTCATCTTGATAGGCTGGGGTTTCCAGCAGCATTTGTT 1015

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QY 191 AlaValTrrpValGlyValAlaArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSer 200
Db 1016 GCAGCATGGCTGTGGCAGCAGCAACTCTGGGTGATGCGAGGTCTGGGAATTAGTGCT 1075
QY 201 GlyHisLysLysTrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPhelile 220
Db 1076 GGAGCATCAAGTGAATTTATCAACACCGATCTTAGCAGCTATTGGGCTGAATTTATT 1135
QY 221 LeuPhelileAsnIleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArg 240
Db 1136 CTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGAGACCAATGCGATTGGG 1195
QY 241 CysAspThrArgGlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeu 260
Db 1196 CATCACACAGGAAGCAATACAGGAACCTGGCAAACTGCACACTGGTCTGCTCCTAGTC 1255
QY 261 PheGlyValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeu 280
Db 1256 TTTGGAGTGCATTACATCGTGTCTGATGCTGCTGCTCACTCC---TTCACCTGGGCTCGG 1312
QY 281 TrpGlnIleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAla 300
Db 1313 TGGAGATCCGATGCACTGCTGAGCTCTCTTCAACTCTTTCAGGGTTCTTTTGTGCT 1372
QY 301 IleIleTyrCysPheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArg 320
Db 1373 ATCATCTACTGCTACTGCAATGGAGGTTTCAGGACAGAGGTGAAGAAGATGTGGAGTCGG 1432
QY 321 TrpThrLeuAlaLeuAspPheLysArgLysAlaArgSerGlySer----- 335
Db 1433 TGGATCTCTCGGTGGATCGAAGAGGACACCGCATGTGGACCGCGAGATGGCGTCA 1492
QY 336 -----SerSerTyrSerTyrGlyProMetValSerHisThrSer 348
Db 1493 GTGCTCACCAACCGTGACGACACAGCAGCAGCAGTCCAGGTGGCGGCCAGCACAGC 1552
QY 349 ValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerProArgLeuProPro 368
Db 1553 ATGTGCTTATC-----TCTGGCAAGCTGCAAGATCGCCAGCAGACAGCCT--- 1600
QY 369 AlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGlyAlaProAlaThr 388
Db 1601 -----GACAGCCATCATCTTTACCTGCTATGTCTGGAGTAAC-----TCA 1642
QY 389 GluThrGluThrLeuPro 394
Db 1643 GAGCAGGACTGCCTGCCA 1660
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## RESULT 13

```
US-08-468-011A-1
; Sequence 1, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
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## SOFTWARE: WORD PERFECT 5.1

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2003 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-468-011A-1
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## Alignment Scores:

Pred. No.:	8.84e-101	Length:	2003
Score:	1036.00	Matches:	208
Percent Similarity:	71.23%	Conservative:	52
Best Local Similarity:	56.99%	Mismatches:	87
Query Match:	45.38%	Indels:	19
DB:	3	Gaps:	5

US-09-869-565-2 (1-435) x US-08-468-011A-1 (1-2003)

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QY 26 GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAlaSer 45
Db 504 GAATTCGTGTAACGCTCTATGTAATGTATACCGTTGGCTACTCCATCTCTTTGGTTCC 563
QY 46 LeuThrValAlaValLeuIleAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
Db 564 TTGGCTGGGTATCTCATCTGGTTACTTCAGACGATTCGATTCGACATTCGACATGGAACATAT 623
QY 66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLysAsp 85
Db 624 ATCCACATGCATTTATTGTGCTTTTCATGCTGAGAGCTACAGCATCTTTGTCAAAGAC 683
QY 86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
Db 684 AGAGTAGTCCATGCTCACAAGAGTAAAGAGGTGGAGTCCCTA----- 728
QY 106 HistIleAlaGlnValProProAlaAlaAlaValGly----- 121
Db 729 -----ATAATGCGAGTACCCCAAAATTCATTTGAGGCAACTTCTGTGGACAAATCA 782
QY 122 ---TyrAlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyr 140
Db 783 CAATATATCGGTGCAAGATTGCTGTTGATGTTTATTACTTCTCGCTACAAATAT 842
QY 141 TyrTrpIleLeuValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSer 160
Db 843 TATTGGATCTCGTGGAGGCTCTCTACCTGCATAATCTCATCTTTGTGGCTTCTTTTCG 902
QY 161 GluLysLysTyrLeuTrrpGlyPheThrIlePheGlyTrrpGlyLeuProAlaValPheVal 180
Db 903 GACACAAATACCTGTGGGCTTCATCTGTATAGCTGGGGTTTCCAGCAGCATTTGTT 962
QY 181 AlaValTrrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSer 200
Db 963 GCAGCATGGGCTGTGGCAGCAGCACTCTGGCTGATCGAGGTGCTGGGAATTAGTGCT 1022
QY 201 GlyHisLysLysTrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPhelile 220
Db 1023 GGAGCATCAAGTGAATTTATCAAGCAGCAGCTCTTAGCAGCTATTGGGCTGAATTTATT 1082
QY 221 LeuPhelileAsnIleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArg 240
```



GENERAL INFORMATION:  
APPLICANT: Soppet, Daniel R  
APPLICANT: Yi, Li  
APPLICANT: Rosen, Craig A  
APPLICANT: Ruben, Steven  
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor  
TITLE OF INVENTION: HLDG74  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
ADDRESSEE: Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: NJ  
COUNTRY: USA  
ZIP: 07068-1739  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07085  
FILING DATE: 05-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-393  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2003 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 90..1712  
PCT-US95-07085-1

Alignment Scores:  
Pred. No.: 8.84e-101 Length: 2003  
Score: 1036.00 Matches: 208  
Percent Similarity: 71.23% Conservative: 52  
Best Local Similarity: 56.99% Mismatches: 87  
Query Match: 45.38% Indels: 19  
Db: 5 Gaps: 5

US-09-869-565-2 (1-435) x PCT-US95-07085-1 (1-2003)

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Qy      26 GluValPheAspArgLeuGlyMetIleThrValGlyTyrSerMetSerLeuAlaSer 45
Db      504 GAATTCGTGAACGCTCTATGATGATATACCGTTGGCTACTCCATCTCTTTGGTTCC 563

Qy      46 LeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsnTyr 65
Db      564 TTGGCTGTGGCTATTTCATCATTTGGTTACTTCAGACGATTGCATTGGCACTAGGACTAT 623

Qy      66 IleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIysAsp 85
Db      624 ATCCACATGCATTTATTGTGCTTTTCATGCTTTCATGAGAGCTACAAGCATCTTTGTCAAAGAC 683

Qy      86 AlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluLeu 105
Db      684 AGAGTAGTCCATGCTCACATAGGAGTAAAGAGGTGGAGTCCCTA----- 728

Qy      106 HisIleIleAlaGlnValProProProAlaAlaAlaValGly----- 121
Db      729 -----ATAATGCAGATGATGCCCAAAATTCATTGAGGCAACTTCTGTGGCAACATCA 782
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```
Qy      122 ---TyrAlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyr 140
Db      783 CAATATATCGGGTGCAGATTGCTGTGTGATGTTATTATTACTTCTGGCTACAAATAT 842

Qy      141 TyrTrpIleLeuValGluGlyLeuTyrIleuHisSerLeuIlePheMetAlaPhePheSer 160
Db      843 TATTGGATCCTGGTGAAGGCTCTACCTGATATATCATCTTTGTGGCTTCTTTTCG 902

Qy      161 GluIysTyrLeuTyrPheThrIlePheGlyTrpGlyLeuProAlaValPheVal 180
Db      903 GACACCAATACCTGTGGGCTTTCATCTGTAGCTGGGGTTTCCAGCAGCATTTGTT 962

Qy      181 AlaValTrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSer 200
Db      963 GCAGCATGGGCTGTGGCAGCAGCAACTCTGGCTGATCGAGGTGCTGGGAACTTAGTGT 1022

Qy      201 GlyHisIysTyrTrpIleGlnValProIleLeuAlaSerValValLeuAsnPheIle 220
Db      1023 GGAGCATCAAGTGATTTATCAAGCACCGATCTTAGCAGCTATTGGGCTGAATTTATT 1082

Qy      221 LeuPheIleAsnIleIleArgValLeuAlaThrIysLeuArgGluThrAsnAlaGlyArg 240
Db      1083 CTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGAGACCAATGCAGTTGG 1142

Qy      241 CysAspThrArgGlnGlnTyrArgIysLeuLeuArgSerThrLeuValValProLeu 260
Db      1143 CATGACACAGAAAGCAATACAGAAACTGGCCAAATCTGGAGACCAATGCAGTTGGT 1202

Qy      261 PheGlyValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeu 280
Db      1203 TTTGAGTGCATTACATCGTTTCTGTGCTGCTGCTCACTCC---TTCACTGGGCTCGGG 1259

Qy      281 TrpGlnIleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAla 300
Db      1260 TGGGAGATCCGATGCATGCTGAGCTCTTCTCAACTCTTTCAAGGTTTCTTTGTGTCT 1319

Qy      301 IleIleTyrCysPheCysAsnGlyGluValGlnAlaGluIleArgIysSerTrpSerArg 320
Db      1320 ATCATCTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAGATGTGGAGTCGG 1379

Qy      321 TrpThrLeuAlaLeuAspPheIysArgIysAlaArgSerGlySerSerTyr---Ser 339
Db      1380 TGAATCTCTCCGTGGACTGGAAAAGGACACCGCCATGTGGCAGCCGAGATGGCGCTCA 1439

Qy      340 TyrGlyProMetValSerHisThrSerValThrAsnValGlyProArgAlaGly----- 357
Db      1440 GTGCTCACCACTGGTGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1499

Qy      358 -----LeuSerLeuProLeuSerProArgLeuProAlaThrThrAsnGlyHisSer 375
Db      1500 TGGTGTCTATCTCTGGCAAGATGCAAGATCGGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1558

Qy      376 GlnLeuProGlyHis 380
Db      1559 ACTTTACCTGGCTAT 1573
```

Search completed: November 24, 2004, 06:11:01  
Job time : 136 secs

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XX (GEO) GEN HOSPITAL CORP.  
 XX Gardella TJ, Kronenberg HM, Potts JT;  
 XX WPI; 2000-465971/40.  
 DR P-PSDB; AAB07529.  
 XX  
 PT New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a  
 PT deletion of the extracellular amino-terminus ligand binding domain,  
 PT useful in screening assays for identifying agonists and antagonists of  
 PT PTH receptor activity.  
 XX  
 PS Claim 2; Fig 1; 81pp; English.  
 XX  
 CC The present sequence encodes a mutant parathyroid hormone (PTH) receptor,  
 CC designated rdeltaNt. The polypeptide is characterized by a deletion of  
 CC the extracellular amino-terminus ligand binding domain. The receptor has  
 CC a minimal domain for ligand binding and is, therefore, useful in  
 CC screening assays designed for the identification of agonists and  
 CC antagonists of PTH receptor activity  
 XX  
 SQ Sequence 1320 BP; 238 A; 402 C; 373 G; 307 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1,21e-193 Length: 1320  
 Score: 2283.00 Matches: 435  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

US-09-869-565-2 (1-435) x AAAS8932 (1-1320)

QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuLeuLeuLeuLeuSer 20  
 DB 1 ATGGGGGGCCCGGATCGCAGCCAGCCGCTGGCGCTCTACTCTGCTGCCAGTCTCAGC 60  
 QY 21 SerAlaTyrAlaLeuGluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSer 40  
 DB 61 TCGGCATATGCGTGGAGGTATTGACCGCTAGGCATGATCTACACCGTGGGATCTCC 120  
 QY 41 MetSerLeuAlaSerLeuThrValAlaValLeuLeuLeuAlaTyrPheArgAlaLeuHis 60  
 DB 121 ATGTCTCTGCTCCCTCCACGGTGGCTGCTGCTATCTCTGCTTATTTAGCGGCTGCAC 180  
 QY 61 CysThrArgAsnTyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSer 80  
 DB 181 TGCACGCGCAACTACATCCACATGCATGTTCCTGCTGTTATGCTGCGCGCGGAGC 240  
 QY 81 IlePheValIysAspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeu 100  
 DB 241 ATCTTGTGAAGACGCTGTGCTCTACTCTGCTTACGCTGGATGAGCGCGGCGCTC 300  
 QY 101 ThrGluGluGluLeuHisIleAlaGlnValProProAlaAlaAlaAlaVal 120  
 DB 301 ACAGAGGAAGATTGCATCTGCGCAGGTGCCACTCTGCGCGCGCTGCGCGCTA 360  
 QY 121 GlyTyrAlaGlyCysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyr 140  
 DB 361 GGCTACGCTGCTGCGCGGGTGCACCTTCTCTCTACTTCTCTCTCTCTCTCTCTCTCT 420  
 QY 141 TyrTrpIleLeuValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPheSer 160  
 DB 421 TACTGGATCTGGTGGGGGCTGATCTTGACAGCGCTCATCTCTCTCTCTCTCTCTCTCT 480  
 QY 161 GluIysIysTyrLeuTyrPheThrIlePheGlyTyrGlyLeuProAlaValPheVal 180  
 DB 481 GAGAGGAAGTACCTGTGGGCTTCCACCATCTTTGGCTGGGCTTACCGCTGTCTCTGTG 540  
 QY 181 AlaValTrpValGlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSer 200  
 DB 541 GCTGTGTGGTGGT 600

QY 201 GlyHisIysIysTrpIleIleGlnValProIleuAlaSerValValLeuAsnPheIle 220  
 DB 601 GGGCACAAGAAGTGGATCATCCAGGTGCCCATCTGTCATCTGTGTGCTCAACTTCATC 660  
 QY 221 LeuPheIleAsnIleIleArgValLeuAlaThrIysLeuArgGluThrAsnAlaGlyArg 240  
 DB 661 CTTTATTATCAACATCATCCGGGTGCTTGCACCTAAGCTTCGGGAGCAATCGGGCGG 720  
 QY 241 CysAspThrArgGlnGlnTyrArgIysLeuLeuLeuLeuLeuLeuValLeuValProLeu 260  
 DB 721 TGTGACACCAAGGAGCAGTACCGAAGTGTCTCAGGTCCACGTTGGTGTCTGTGCGCTC 780  
 QY 261 PheGlyValHisTyrThrValPheMetAlaLeuProTyrThrGluValSerGlyLeu 280  
 DB 781 TTTGGTGTGCATACACCGCTTTCATGGCTTCCCGTACACCGAGGTCTCAGGACATG 840  
 QY 281 TrpGlnIleGlnMetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAla 300  
 DB 841 TGGCAGATCCAGATGCATTTATGAGATGCTCTTCAACTCCTTCCAGGGATTTTGTGTC 900  
 QY 301 IleIleTyrCysPheCysAsnGlyGluValGlnAlaGluIleArgIysSerTrpSerArg 320  
 DB 901 ATCATATACTGTTTCTGCAATGCTGAGTGCAGGCAGAGATTAGGAAGTCATGGAGCGC 960  
 QY 321 TrpThrIleAlaLeuAspPheIysArgIysAlaArgSerGlySerSerTyrSerTyr 340  
 DB 961 TGGACATGCTGGCTTGGACTTCAAGCGCAAGCAGCAGAGTGGAGTAGCAGCTACAGCTAT 1020  
 QY 341 GlyProMetValSerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeu 360  
 DB 1021 GGCCCAATGTTGCTCACACGAGTGTGACCAATGTGGCCCCCGTGCAGACTCAGCCTC 1080  
 QY 361 ProLeuSerProArgLeuProAlaThrThrAsnGlyHisSerGlnLeuProGlyHis 380  
 DB 1081 CCCTCTCAGCCCCGCTGCTCTCTGCTTACCGCTCTCTGCTCAGGCTGGATGAGGAGGCT 1140  
 QY 381 AlaIysProGlyAlaProAlaThrGluThrGluThrLeuProValThrMetAlaValPro 400  
 DB 1141 GCCAAGCCAGGGGCTCCAGCCACTGAGACTGAAACCTTACAGTCACTATGGCGGTTCCC 1200  
 QY 401 LysAspAspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySer 420  
 DB 1201 AAGGACGATGATTCCTTAAACGCTCTCTGCTCAGGCTGGATGAGGAGGCTCCGGTCT 1260  
 QY 421 AlaArgProProProLeuLeuGlnGlyTyrGluThrValMet 435  
 DB 1261 GCAGCGCGCTCTCCATTGTTGCAGGAAGGATGGAAACAGTCATG 1305

RESULT 2  
 AAAS1732  
 ID AAAS1732 standard; DNA; 1341 BP.  
 AC AAAS1732;  
 DT 31-OCT-2000 (first entry)  
 XX Tethered PTH-1 receptor, Tether1, coding sequence.  
 XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
 KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.  
 XX Rattus sp.  
 OS Synthetic.  
 OS Chimeric.  
 XX Key Location/Qualifiers  
 FH 1. .1341  
 FT CDS /\*tag= a  
 FT /product= "Tether-1"  
 XX WO200039278-A2.  
 XX





XX 25-MAR-2003 (revised)  
 DT 18-MAY-1996 (first entry)  
 XX  
 XX  
 DE Rat bone PTH/PTHrP receptor cDNA clone R15B.  
 XX  
 DE Parathyroid hormone; receptor; parathormone; PTH;  
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;  
 KW hypercalcaemia; hypocalcaemia; cancer; transgenic animal;  
 KW transgenic fowl; ds.  
 XX  
 XX  
 OS Rattus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 73..1848  
 FT /\*tag= a  
 XX  
 XX US5494806-A.  
 PN  
 XX 27-FEB-1996.  
 PD  
 XX  
 XX 06-APR-1992; 92US-00864475.  
 PF  
 XX  
 PR 05-APR-1991; 91US-00681702.  
 XX  
 XX (GEO) GEN HOSPITAL CORP.  
 PA  
 XX Potts JT, Juppner H, Segre GV, Schipani E, Kronenberg HM;  
 PI Abou-Samra A;  
 XX WPI; 1996-139028/14.  
 XX P-PSDB; AAR92277.  
 DR  
 XX  
 XX DNA encoding vertebrate parathyroid hormone receptor - useful for  
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia, cancer  
 PT etc.  
 PT  
 XX  
 XX Claim 1; Fig 3A-3E; 64pp; English.  
 PS  
 CC A cDNA clone (AAT15947), designated R15B ATCC 68571, codes for a rat  
 CC parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)  
 CC receptor (AAR92277). To obtain R15B, a rat osteosarcoma ROS 17/2.8 cDNA  
 CC library in pcDNA1 was used to transfect COS cells, and transfectants were  
 CC selected for ability to bind labelled PTH. Recombinant receptor is  
 CC produced in vector/host cell systems. The host cells can be used for  
 CC diagnostic measurement of PTH serum levels. Transgenic chickens that  
 CC overexpress the receptor in their oviduct lay eggs of higher calcium  
 CC content. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.57e-185 Length: 2051  
 Score: 2195.00 Matches: 435  
 Percent Similarity: 73.60%  
 Best Local Similarity: 73.60% Conservative: 0  
 Query Match: 96.15% Mismatches: 0  
 DB: 2 Indels: 156  
 Gaps: 1

US-09-869-565-2 (1-435) x AAT15947 (1-2051)

QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuLeuLeuLeuLeuSer 20  
 DB 73 ATGGGGGCGCGCGGATGCGACCCAGCTGGCGCTCTCTCTGCTGCCAGTGTCTCAGC 132  
 QY 21 SerAlaTyrAlaLeu----- 25  
 DB 133 TCAGCATATGCGTGGTGGATGGGACGATGCTTTTACCAAGAGAACAGATTTCCTG 192  
 QY 25 ----- 25  
 DB 193 CTGACCGGTGCCAGGCGCAATGTGACAGTGCTCAAGGAAGTTCTGTGCACAGCAGCC 252

QY 25 ----- 25  
 DB 253 AACATAATGAGTTCAGACAAGGGCTGGACACAGCATCTAGTTCAGGAAGCCAGGAAA 312  
 QY 25 ----- 25  
 DB 313 GAGAGGCATCGGGAAGTTCTACCTGAGTCTAAAGAGAGAACAAGGACGTGCCACCGGC 372  
 QY 25 ----- 25  
 DB 373 AGCAGCGCAGAGGGCGTCCCTGTCTGCCGAGTGGGACAAACATCGTTTGTGCGCCATTA 432  
 QY 25 ----- 25  
 DB 433 GGGGACACCGGTGAAGTGGTGAGTACCTTTGCCGATTACATTTATGACTTCAATCAC 492  
 QY 25 ----- 25  
 DB 493 AAAGGCCATCGCTACAGACGCTGTGACCGCAATGGCAGCTGGGAGGTGTTCCAGGGCAC 552  
 QY 25 ----- 25  
 DB 553 AACCGGACGTGGGCGCACTACAGCGAGTGCTCAAGTTTCATGACCAATGAGACGCGGAA 612  
 QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44  
 DB 613 CGGAGGTATTTGACCGCCTAGGATGATCTACACCGTGGATACTCATGTCTCTGCC 672  
 QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64  
 DB 673 TCCTCAGCGTGGCTGTGCTCATCTGGCCTATTTAGCGCGCTGCACATGCACGCGAAC 732  
 QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIys 84  
 DB 733 TACATCCACATGCACATGTTCTCTGCTTTATGTGCGCGCGGAGCATCTTCGTGAAG 792  
 QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104  
 DB 793 GAGCTGTGCTTACTCTTGGCTTACGCTGGATGAGGCCGCGCTTCACAGAGGAAGAG 852  
 QY 105 LeuHisIleIleAlaGlnValProProAlaAlaAlaAlaAlaValGlyTyrAlaGly 124  
 DB 853 TTGCACATCATCGCGAGTGCCACCTCCCGCGCGCTGCGCGCTAGCTACGCTGGC 912  
 QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleu 144  
 DB 913 TGGCGGTGGCGGTGACCTTCTCTCTACTTCTGCTACCACTACTACTGATCTG 972  
 QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysTyr 164  
 DB 973 GTGGAGGGGTGTACTTGCACAGCTCATCTTATGGCCCTTTTCTCAGAGAAAGTAC 1032  
 QY 165 LeuTrpGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTrpVal 184  
 DB 1033 CTGTGGGGCTTCCACCATTTTGGCTGGGTCTACCGGCTGCTTCTGCTGGTGTGGGTC 1092  
 QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLys 204  
 DB 1093 GGTGTACAGCAACCTTGGCCAAACACATGGGTGGGATCTGAGCTCCGGGACAAAG 1152  
 QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224  
 DB 1153 TGGATCATCCAGGTGCCCATCTTGGCATCTGTGTGCTCAACTTCATCTTATCAAC 1212  
 QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244  
 DB 1213 ATCATCGGTGTCTGGCACTTAAGCTTCGGGAGACCAATGGGCGCGGTGTGACACGAG 1272  
 QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264  
 DB 1273 CAGCAGTACCGAAGCTGTGCTCAGTCCAGTGTGTGCTGTGCGCTCTTTGGTGTCCAC 1332  
 QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284

Db 1333 TACACCGTCTTCATGCGCTGCGTACACCGAGGTCTCAGGACATTTGGCAGATCCAG 1392  
QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys 304  
Db 1393 ATGCATTATGAGATGCTCTTCACTCTTCCAGGGATTTTGTGGCCATCATATCTGT 1452  
QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324  
Db 1453 TTCTGCNATGGTGAGGTGACGAGCAGAGATTAGAGTCTAGGAGCCGCTGGACACTGGCG 1512  
QY 325 LeuAppPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344  
Db 1513 TTGGACTTCAAGCGCAAGACGACGAGTGGAGTAGCAGCTACAGCTATGGCCCAATGGTG 1572  
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364  
Db 1573 TCTCACACAGTGTGACCAATGGGCCCCCGGTGAGGAGCTCAGGCTCCCTCAGCCCC 1632  
QY 365 ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384  
Db 1633 CGCTTGCTCTCTGCGCACTACCAATGGCCACTCCAGCTGCTGGCCATGCCAAGCCAGGG 1692  
QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspAspGly 404  
Db 1693 GCTCCAGCACTGAGACTGAAACCCCTACCACTACTATGGCGGTTCCCAAGACGATGGA 1752  
QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArgProPro 424  
Db 1753 TTCCCTTAACGGCTCCTGCTCAGGCTGGATGAGAGGCTCCGGGTCTGCGGCGCGCT 1812  
QY 425 ProLeuLeuGlnGlyTyrProGluThrValMet 435  
Db 1813 CCATTGTTCAGGAAGGATGGGAACAGTCATG 1845

RESULT 4  
AAV08390  
ID AAV08390 standard; DNA; 2051 BP.  
XX AC AAV08390;  
XX DT 08-FEB-1999 (first entry)  
XX DE Parathyroid hormone receptor R15B coding sequence.  
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;  
XX KW PTH-related hypercalcaemia; rat; ds.  
XX OS Rattus sp.  
XX FH Key Location/Qualifiers  
XX FT CDS 73..1848  
XX FT /\*tag= a  
XX FN US5840853-A.  
XX PD 24-NOV-1998.  
XX PF 06-JUN-1995; 95US-00471494.  
XX PR 05-APR-1991; 91US-00681702.  
XX PR 06-APR-1992; 92US-00864475.  
XX PA (GENO ) GEN HOSPITAL CORP.  
XX PI Abou-Samra A, Juppner H, Potts JT, Segre GV, Schipani E;  
XX PI Kronenberg HM;  
XX DR WPI; 1999-034124/03.  
XX DR P-PSDB; AAW73316.  
XX PT Antibody to parathyroid hormone receptor - for diagnostic or therapeutic use.

XX Claim 6; Fig 3; 63pp; English.  
XX This sequence encodes the rat parathyroid hormone (PTH) receptor R15B, which is targeted by the antibody of the invention. The antibody of the invention is immunoreactive with naturally occurring human, rat or opossum PTH receptor. The antibody is useful for treating disorders characterised by overstimulation of PTH receptors by their ligand and for the diagnosis of PTH-related hypercalcaemia  
XX Sequence 2051 BP; 429 A; 575 C; 616 G; 431 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1.57e-185 Length: 2051  
Score: 2195.00 Matches: 435  
Percent Similarity: 73.60% Conservative: 0  
Best Local Similarity: 73.60% Mismatches: 0  
Query Match: 96.15% Indels: 156  
DB: 2 Gaps: 1

US-09-869-565-2 (1-435) x AAV08390 (1-2051)  
QY 1 MetGlyValAlaArgIleAlaProSerLeuAlaLeuLeuLeuCysCysProValLeuSer 20  
Db 73 ATGGGGGGCGCCCGGATGCGACCCAGCTGGCGCTCTACTCTGCTGCCAGTGTCTCAGC 132  
QY 21 SerAlaTyrAlaLeu----- 25  
Db 133 TCCGCATATGCGTGGTGGATGCGGACGATGCTTTTACCAAGAGAACACAGATTTCCTGTG 192  
QY 25 ----- 25  
Db 193 CTGCACCGTGGCCAGCGCAATGTGCAAGCTGTCTCAAGGAAGTTCTGCACACAGCAGCC 252  
QY 25 ----- 25  
Db 253 AACATAATGGAGTCAGACAAGGGCTGGACACAGCATCTACGTCAAGGAAGCCAGGAAA 312  
QY 25 ----- 25  
Db 313 GAGAAGGCATCGGAAAGTTCTACCTGAGTCTAAAGAGACAAAGACGTGCCACCGCC 372  
QY 25 ----- 25  
Db 373 AGCAGCGCAGAGGCGTCCCTGTCTGCCGAGTGGGACAACATCGTTTGTGGCCATTA 432  
QY 25 ----- 25  
Db 433 GGGGCACACAGTGAAGTGGTGGCAGTACCTTGTCGCGATTACATTTATGACTTCAATCAC 492  
QY 25 ----- 25  
Db 493 AAAGGCCATGCTACAGACGCTGTGACCGCAATGCGACGTGGGAGGTGGTTCCAGGGCAC 552  
QY 25 ----- 25  
Db 553 AACCGGACGTGGGCCAACTACAGCGAGTGCCTCAAGTTTCATGACCAATGAGACGGGAAA 612  
QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44  
Db 613 CGGAGAGTATTTGACCGCTTAGGCATGATCTACACCGTGGGATACTCCATGTCTCTGCC 672  
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64  
Db 673 TCCCTCACGGTGGTGTGCTCATCTGGCTATTTAGGGCGCTGCACTGCACGCGCAAC 732  
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84  
Db 733 TACATCCACATGCACATGTTCTCTGCTGTTATGCTGCGCGCGGAGCATCTTCGTGAAG 792  
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGlu 104  
Db 793 GACGCTGTGCTCTACTCTGGCTTCACGCTGGATAGGCGCGGCGCTCACAGAGNAGAG 852



Qy	21	SerAlaTyrAlaLeu-----	25
Db	133		192
		TCCGATATGGCTGGTGGATCGGACGATGCTTTTACAAAGAGAAACAGATTTCCTG	
Qy	25	-----	25
Db	193	CTGCACCGTGCCAGGCGCAATGTGACAAAGTGTCTCAAGCTGTCTCAAGGAAGTTCTGCACACAGCAGCC	252
Qy	25	-----	25
Db	253	AACATAATGGAGTCAGACAAGGCTGGACACAGCATCTACGTCAAGGAAGCCCAAGGAAA	312
Qy	25	-----	25
Db	313	GAGAAAGCATCGGAAAGTTCTTACCTGAGTCTTAAAGAGAAACAAGACGTGCCACCGGC	372
Qy	25	-----	25
Db	373	AGCAGGCGCAGAGGCGTCCCTGTCTGCCGAGTGGGACAACATCGTTTGTGTGGCCATTA	432
Qy	25	-----	25
Db	433	GGGCAACAGGTGAAGTGGTGCGAGTACCTTGTCCCATTACATTTATGACTTCAATCAC	492
Qy	25	-----	25
Db	493	AAAGGCCATGCTTACAGACGCTGTGACCGCAATGCGAGCTGGAGGTGGTTCCAGGGCAC	552
Qy	25	-----	25
Db	553	AACCGGACGTGGCCAACTACAGCGAGTGCCCTCAAGTTCATGACCAATGAGACGCGGAA	612
Qy	26	---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla	44
Db	613	CGGAGGTATTTGACCGCTAGGCATGATCTACACCGTGGGATACTCCATGCTCTCTGCC	672
Qy	45	SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn	64
Db	673	TCCCTACGGTGGGTGTGCTCATCTGGCCTATTTTAGCGCGCTGCATGCAACGCGAAC	732
Qy	65	TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValIys	84
Db	733	TACATCCACATGCACATGTTCTCTGCTGTATGTGCGCGCGCGAGCATCTCTCGTAAG	792
Qy	85	AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu	104
Db	793	GACGCTGTGCTTACTCTGGCTTACGCTGATGAGCGCGAGCGCTCCACAGAGAAAG	852
Qy	105	LeuHisIleIleAlaGlnValProProProAlaAlaAlaValGlyTyrAlaGly	124
Db	853	TTGCACATCATCGCGCAGGTGCCACCTCCGCGCGCGCTGCCGCGTAGGCTACGCTGGC	912
Qy	125	CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu	144
Db	913	TGCGCGTGGCGTGCACCTTCTTCTTACTTCTGGCTACCAACTACTACTGTGATTCG	972
Qy	145	ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLeuLysTyr	164
Db	973	GTGAGGGGCTGTACTTGCACAGCCTCATCTTCATGCGCTTTTCTCAGAGAAGAGTAC	1032
Qy	165	LeuTrpGlyPheThrIlePheGlyTyrPGLyLeuProAlaValPheValAlaValTrpVal	184
Db	1033	CTGTGGGGCTTCCACATCTTTGGCTGGGGTCTACCGCGTGTCTTCGTGGCTGTGTGGGC	1092
Qy	185	GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLys	204
Db	1093	GGTGTACAGACAACCTTGGCCAAACACTGGGTGCTGGGATCTCGAGCTCGGGCACACAAG	1152
Qy	205	TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn	224
Db	1153	TGGATCATCAGGTGCCCATCTGGCATCTGTGTGTCTCAACTTCATCTTTTATCAAC	1212
Qy	225	IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg	244

Db	1213	ATCATCCGGGTGCTTGCCCACTAAGCTTCGGGAGACCAATCGGCGCGGTGTGACACCAGG	1272
QY	245	GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis	264
Db	1273	CAGCAGTACCGGAAGCTGCTCAGGTCCACGTTGGTGTGCTGCGCGCTCTTTGGTGTCCAC	1332
QY	265	TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGln	284
Db	1333	TACACCGTCTTCATGGCTTGCCGTACCGAGGTCTCAGGACATTTGTGGCATCATATACTGT	1392
QY	285	MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys	304
Db	1393	ATGCATTATGAGATGCTCTTCAACTCTCCAGGATTTTTTTGTGGCATCATATACTGT	1452
QY	305	PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla	324
Db	1453	TTCTGCAATGGTGGAGTGCAGGCAGAGATTAGGAAGTCATGGAGCCGCTGGACACTGGCG	1512
QY	325	LeuAspPheLysArgLysAlaAatqSerGlySerSerTyrSerTyrGlyProMetVal	344
Db	1513	TTGACTTCAAGCCCAAGCACGAACTGGAGTAGCAGCTACAGCTATGCCCAATGGTG	1572
QY	345	SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro	364
Db	1573	TCTCACACGAGTGTGACCAATGTGGGCCCCCGTGCAGAGCTCAGCCTCCCCCTCAGCCCC	1632
QY	365	ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly	384
Db	1633	CGCTGCTGCTCTGTCACCTACCAATGGCCACTCCCGAGCTGCTGGCCATGCCAAGCCAGG	1692
QY	385	AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspGly	404
Db	1693	GCTCAGCCACTGAGACTGAACCTTACCAGTCACTATGGCGGTCTCCAAGGACGATGA	1752
QY	405	PheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArgProPro	424
Db	1753	TTCTTAAACGGCTCTCTCTCAGGCTGGATGAGGAGGCTCCGGTCTGCGGCGCGCT	1812
QY	425	ProLeuLeuGlnGluGlyTyrGluThrValMet	435
Db	1813	CCATTGTTGCAGGAAGGATGGAAACAGTCATG	1845
RESULT	6		
AAQ29606			
ID	AAQ29606	standard; cDNA; 2051 BP.	
XX	AC	AAQ29606;	
XX	DT	25-MAR-2003 (revised)	
DT	DT	16-MAR-1993 (first entry)	
XX	XX		
DE	Rat bone PTHrP receptor clone, R15B.		
XX			
KW	Parathyroid hormone; related protein; calcium; antagonist; antibodies;		
KW	hypercalcaemia; ss.		
XX			
OS	Rattus rattus.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	73..1848	
FT		/*tag= a	
XX			
PN	W09217602-A1.		
XX			
PD	15-OCT-1992.		
XX			
PF	06-APR-1992; 92WO-US002821.		
XX			
PR	05-APR-1991; 91US-00681702.		
XX			
XX	(GEHO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.		
XX			



QY 365 ArgLeuProAlaThrThrBenglyHisSerGlnLeuProGlyHisAlaLysProGly 384  
 Db 1633 CCGCTGCTTCCTGCGCCATACCAATGCCACTCCAGCTCCCTGGCCATGCCAAGCCAGGG 1692  
 QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspAspGly 404  
 Db 1693 GCTCCAGCCACTGAGACTGAAACCCCTACAGTCATCTATGGCGGTCCCAAGGACATGGA 1752  
 QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluGluAlaSerGlySerAlaArgProPro 424  
 Db 1753 TTCCTTAACGGCTCCTGCTCAGGCTGGATGAGGAGGCTCCGGCTCTGCGCGCGCGCT 1812  
 QY 425 ProLeuLeuGlnGluGlyTrpGluThrValMet 435  
 Db 1813 CCATTGTTGCAGGAAGATGGGAACAGTCATG 1845

## RESULT 7

ABT42039  
 ID ABT42039 standard; DNA; 2065 BP.

XX AC ABT42039;

XX DT 26-JUN-2003 (first entry)

XX DE Toxicity modelling related rat gene SEQ ID No 1741.

XX KW Toxic effect; gene expression profile; renal toxicity; toxicity marker;  
 KW database; drug screening; toxicity assay; rat; ds.

XX OS Rattus norvegicus.

XX PN WO200295000-A2.

XX PD 28-NOV-2002.

XX PF 22-MAY-2002; 2002WO-US016173.

XX PR 22-MAY-2001; 2001US-0292335P.

XX PR 13-JUN-2001; 2001US-0297523P.

XX PR 19-JUN-2001; 2001US-0298925P.

XX PR 10-JUL-2001; 2001US-0303807P.

XX PR 10-JUL-2001; 2001US-0303808P.

XX PR 10-JUL-2001; 2001US-0303810P.

XX PR 28-AUG-2001; 2001US-0315047P.

XX PR 27-SEP-2001; 2001US-0324928P.

XX PR 22-OCT-2001; 2001US-0330462P.

XX PR 01-NOV-2001; 2001US-0330867P.

XX PR 21-NOV-2001; 2001US-0331805P.

XX PR 06-DEC-2001; 2001US-0336144P.

XX PR 19-DEC-2001; 2001US-0340873P.

XX PR 21-FEB-2002; 2002US-0357842P.

XX PR 21-FEB-2002; 2002US-0357843P.

XX PR 15-MAR-2002; 2002US-0357844P.

XX PR 15-MAR-2002; 2002US-0364134P.

XX PR 08-APR-2002; 2002US-0370144P.

XX PR 08-APR-2002; 2002US-0370206P.

XX PR 08-APR-2002; 2002US-0370247P.

XX PR 17-APR-2002; 2002US-0372794P.

XX PR 21-APR-2002; 2002US-0371679P.

XX PA (GENE-) GENE LOGIC INC.

XX PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;

XX WPI; 2003-148464/14.

XX PT Predicting at least one toxic effect of a compound, useful for toxicity  
 PT modeling, comprises preparing a gene expression profile of a tissue or  
 PT cell sample exposed to the compound, and comparing the gene expression  
 PT profile to a database.

XX PS Example 4; Page; 446pp; English.

XX PS

CC The invention relates to a novel method of predicting at least one toxic  
 CC effect of a compound. The method comprises a gene expression profile of a  
 CC tissue or cell sample exposed to the compound, and comparing the gene  
 CC expression profile to a database comprising at least part of the data or  
 CC information given in the specification. The methods are useful for  
 CC predicting at least one toxic effect of a compound, predicting the renal  
 CC toxicity of a compound, or identifying toxicity markers in tissues or  
 CC cells exposed to known renal toxin. The genes are useful as toxicity  
 CC markers in drug screening and toxicity assays, in monitoring disease or  
 CC physiological states, or disease progression. This polynucleotide  
 CC represents a rat DNA sequence relating to the toxic effect database  
 CC described in the specification. NOTE: The sequence data for this patent  
 CC did not form part of the printed specification, but was obtained in  
 CC electronic format directly from the World Intellectual Property  
 CC Organization

XX SQ Sequence 2065 BP; 435 A; 578 C; 617 G; 435 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 8,19e-185 Length: 2065  
 Score: 2187.00 Matches: 434  
 Percent Similarity: 73.43% Conservative: 0  
 Best Local Similarity: 73.43% Mismatches: 1  
 Query Match: 95.80% Indels: 156  
 DB: 10 Gaps: 1

US-09-869-565-2 (1-435) x ABT42039 (1-2065)

QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuLeuLeuSer 20  
 Db 73 ATGGGGCGCCCGCGATCGCACCGCTGCGCTCTACTCTGCTGCCAGTGCTCAGC 132  
 QY 21 SerAlaTyrAlaLeu----- 25  
 Db 133 TCCGCATATGCGCTGGTGGATGCGGACGATGCTTTTACCAAGAGGAACAGATTTCCTG 192  
 QY 25 ----- 25  
 Db 193 CTGCACCGTGCCAGCGCAATGTGACAAGCTGCTCAAGGAAGTTCTGCACACAGCACC 252  
 QY 25 ----- 25  
 Db 253 AACATAATGGAGTCAGACAAGGGCTGGACACACAGCATCTACGTCAGGGAAGCCAGGAAA 312  
 QY 25 ----- 25  
 Db 313 GAGAGGCATCGGGAAGTTCTACCTGAGTCTTAAAGAGAACAAGGACGTCGCCACCGGC 372  
 QY 25 ----- 25  
 Db 373 AGCAGCGCAGAGGGCGTCTGCTGCCGAGTGGGACAACATCGTTTGTGCTGCCATT 432  
 QY 25 ----- 25  
 Db 433 GGGGCACCAAGTGAAGTGGTGGCAGTACCTTGTCCGATTACATTATGACTTCAATCAC 492  
 QY 25 ----- 25  
 Db 493 AAAGGCCATGCCTACAGACGCTGTGACCGCAATGGCAGCTGGGAGGTGTTCCAGGGCAC 552  
 QY 25 ----- 25  
 Db 553 AACCGGACGTGGCCAACTACAGCGAGTGCTCAAGTTTCATGACCAATGAGACCGGGAA 612  
 QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44  
 Db 613 CGGAGAGGTATTTAGCCGCTAGGCATGATCTACACCGTGGGATCACTCATGCTCTCGCC 672  
 QY 45 SerLeuThrValAlaValLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64  
 Db 673 TCCCTCAGGTGGTGTGCTCATCTTGGCCTATTTTAGCGCGGTGCACTGACGCGCAAC 732

QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84  
DB 733 TATATCCACATGCACATGTTCTGTCTATGTCGCGCGCGAGCATCTTCGTGAAG 792  
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGlu 104  
DB 793 GAGCGTGTCTTACTCTGTCTTACGCTGATGAGCGCGAGCGCTTCACAGAGGAGAG 852  
QY 105 LeuHisIleAlaGlnValProProProAlaAlaAlaAlaValGlyTyrAlaGly 124  
DB 853 TTGCACATCATCGCAGAGTGCACCTCGCGCGCGCTGCGCGCTAGGCTACGCTGGC 912  
QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTyrLeu 144  
DB 913 TGCCTGCTGCGGTGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 972  
QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluTyrLysTyr 164  
DB 973 GTGAGGGGCTGTACTTGCACAGCTCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1032  
QY 165 LeuTyrGlyPheThrIlePheGlyTyrGlyLeuProAlaValPheValAlaValTyrVal 184  
DB 1033 CTGTGGGCTTACCATCTTGTGCTGGGTCTACCGCTGTCTTCTGCTGGCTGTGTGGCTC 1092  
QY 185 GlyValArgAlaThrLeuAlaThrGlyCysTyrAspLeuSerSerGlyHisLysLys 204  
DB 1093 GGTGTGAGAGAACCTTGGTCAACACTTGGGTCTGGATCTGAGCTCCGGGCAACAGAG 1152  
QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224  
DB 1153 TGGATCATCAGTGGCCATCTTGGCATCTGTGTGCTCAACTTCATCTTTTATCAAC 1212  
QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244  
DB 1213 ATCATCGGTGCTTGCACATGAGTTCGGGAGACCAATCGGGCGGTGTGACACCGAG 1272  
QY 245 GlnGlyTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264  
DB 1273 CAGCAGTACCGGAGCTGCTCAGTCCACGTTCAGTGTGCTGCTGCTGCTGCTGCTGCTG 1332  
QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTyrGlnIleGln 284  
DB 1333 TACACCGTCTTCATGGCTTGGCTACACGAGGTCTCAGGACATTTGTGGCAGATCCAG 1392  
QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPheValAlaIleIleTyrCys 304  
DB 1393 ATGCATTATGAGATGCTCTTCAACTCTCTCCAGGATTTTTTGTGCTCATCATATCTGT 1452  
QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTyrPheArgTyrThrLeuAla 324  
DB 1453 TTCTGCAATGTTGAGGTGCGAGCAGAGATTAGGAGTCNTGGAGCCCTGGACACTGGCG 1512  
QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344  
DB 1513 TTGAGCTTCAAGCGCAAGCAGCAAGTGGAGTAGCAGTACAGCTATGCGCCCAATGGT 1572  
QY 345 SerHisThrSerValThrAsnValGlyProArgLysLeuSerLeuProLeuSerPro 364  
DB 1573 TCTCACAGAGTGTGACCAATGTGGCCCGCGTCCAGACTCAGCTCCCGCTCAGCGCC 1632  
QY 365 ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384  
DB 1633 CGCTGCTCTCTGCACTACCAATGGCCACTCCAGCTGCTGCGCCATGCCAAGCCAGGG 1692  
QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspAspGly 404  
DB 1693 GCTCCAGCACTGAGCTGAAACCTTACAGTCACTATGGCGGTTCACAGGACGATGGA 1752  
QY 405 PheLeuGlnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProPro 424  
DB 1753 TTCCTTAACGGCTCTGCTCAGGCTGATGAGAGGCGCTCCGGTCTGCGCGCGCGCT 1812  
QY 425 ProLeuLeuGlnGlyTyrGluThrValMet 435

Db 1813 CCATTGTCAGGAGATGGGAACAGTCATG 1845

## RESULT 8

ADO30323

ID ADO30323 standard; cDNA; 1776 BP.

XX ADO30323;

XX 29-JUL-2004 (first entry)

XX Mouse GPCR PTHR1 polynucleotide, SEQ ID NO:1426.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
transgenic mouse; neurological disorder; adrenal gland disorder;  
colon disorder; intestinal disorder; cardiovascular disorder;  
muscular disorder; blood disorder; immune disorder; bone disorder;  
joint disorder; metabolic disorder; nutritive disorder; cancer;  
kidney disorder; liver disorder; lung disorder; breast disorder;  
ovary disorder; uterus disorder; prostate disorder; testis disorder;  
skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;  
cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
murine; gene; ss.

XX Mus musculus.

OS WC2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

XX P-PSDB; ADO29629.

XX Novel mammalian G protein coupled receptors, useful for identifying

XX compounds that modulates diagnosing and treating disease condition

XX associated with GPCR dysfunction e.g. autoimmune diseases, angina

XX pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 1426; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors  
(GPCRs) and nucleic acids encoding them. The invention also relates to  
sequences at least 90% identical to the GPCR proteins and nucleic acids  
of the invention; methods of treating, preventing or diagnosing diseases  
associated with GPCRs of the invention; methods of screening for  
compounds useful in the treatment of GPCR-related diseases; a transgenic  
mouse comprising a GPCR gene of the invention; a mouse comprising a  
mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
from the transgenic mice; kits comprising several mice, each of which has  
a mutation in a different GPCR gene of the invention; and kits comprising  
probes which hybridise to GPCR polynucleotides of the invention. The  
invention further discloses variants of the GPCR polypeptides and vectors  
comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
be used in the diagnosis, treatment or prevention of a wide variety of  
diseases including neurological disorders (e.g., Alzheimer's disease,  
depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
disorders of the adrenal gland; disorders of the colon or intestine  
(e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel



CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a gpCR-encoding  
 CC nucleic acid of the invention. Note: The full sequence data for this  
 CC patent did not form part of the printed specification; those sequences  
 CC not shown were obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX  
 SQ Sequence 1776 BP; 364 A; 519 C; 500 G; 393 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 3e-181 Length: 1776  
 Score: 2146.00 Matches: 426  
 Percent Similarity: 72.42% Conservativity: 2  
 Best Local Similarity: 72.08% Mismatches: 7  
 Query Match: 94.00% Indels: 156  
 DB: 12 Gaps: 1

US-09-869-565-2 (1-435) x ADO30323 (1-1776)

QY 1 MetGlyAlaAlaArgIleAlaProSerLeuAlaLeuLeuLeuLeuLeuLeuLeuSer 20  
 DB 1 ATGGGGACCGCGGATCGCACCGAGCTGGCGCTCTCTCTGCTGCCAGTGTCTCAGC 60  
 QY 21 SerAlaTyrAlaLeu----- 25  
 DB 61 TCCGCATATGGCGTGGTGGAGCGAGAGATGCTTTTACCAAGAGGAACAGATTTCCTG 120  
 QY 25 ----- 25  
 DB 121 CTGCACCGTGCACCGCGCAATGTGACAAGCTGTCTCAAGGAAGTCTGTCACACAGCACC 180  
 QY 25 ----- 25  
 DB 181 AACATAATGGAGTCAGACAAAGGGTGGACTCCAGCATCTACGTGAGGGAAGCCAGGAAA 240  
 QY 25 ----- 25  
 DB 241 GAGAGGCCACGGGAAGTCTACCCCGAGTCTAAAGAGAACAAAGGATGTGCCACCGGC 300  
 QY 25 ----- 25  
 DB 301 AGCAGGCGCGAGGGCGTCCCTGTCTGCAGAGTGGGACACATCGTTTGTGTCGCCATTG 360  
 QY 25 ----- 25  
 DB 361 GGGGACACAGGTGAAGTGGTGGCAGTACCTTGTCCCGATTACATTATGACTTCAACAC 420  
 QY 25 ----- 25  
 DB 421 AAAGGCCATGCCCTACAGACGCTGGCGCGCAATGGCAGCTGGGAGGTGTTCCAGGGCAC 480  
 QY 25 ----- 25  
 DB 481 AACCGGAGCTGGGCCAACTACAGCGAGTGGCTCAAGTTCATGACCAATGAGACTCGGGAA 540  
 QY 26 ---GluValPheAspArgLeuGlyWeileTyrThrValGlyTyrSerMetSerLeuAla 44  
 DB 541 CGGAGGATATTTCACCGCTGGGCATGATCTACACCGTGGGATATTCATGTCTCTTGGC 600  
 QY 45 SerLeuThrValAlaValLeuLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64  
 DB 601 TCCCTCACCGTGGTGTGCTCATCTAGCCTATTTTAGGGGCGTGCACCTGCACGCGCAAC 660  
 QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaAlaSerIlePheValLys 84  
 DB 661 TACATCCACATGCACATGTTCTCTGCTTATGCTGCGCGCGCGAGCACTTCTGTGAAG 720

QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGlu 104  
 DB 721 GACCTGTGCTCTACTCTGGCTTTCACGTGGATGAGCGCGAGCGCTCACGAGGAAGAG 780  
 QY 105 LeuHisIleIleAlaGlnValProProProProAlaAlaAlaAlaValGlyTyrAlaGly 124  
 DB 781 TTGCATATCATCGCGAGGTGCCCGCTCCCGCCCGCTGCCCGCTTGGCTAGCTGCGC 840  
 QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144  
 DB 841 TGCCTGTGGCGGTGACCTTCTCTCTACTCTCTGCTACCACTACTACTGATTCG 900  
 QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysTyr 164  
 DB 901 GTGAGGGAGCTGTACTTACACAGCTCATCTTATGCGCTTTTCTCAGAGAGAAGTAT 960  
 QY 165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184  
 DB 961 CTGTGGGGCTTTCACCATCTTGGCTGGGGTCTGCCGCTGTCTTCTGGCTGTGTGGGTC 1020  
 QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLys 204  
 DB 1021 GGTGTACAGACCACTTGGCCCAACACTGGGTGGTGGACCTGAGCTCTGGGCACAAGAG 1080  
 QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224  
 DB 1081 TGGATCATCCAGGTGCCCATCTGGCATCTGTGTGCTCAACTTCATCTCTTTATCAAC 1140  
 QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244  
 DB 1141 ATCATCCGGGTGTCTGCCACTAAGCTTCGGGAGACCAATCGGCGCGGTGTGACACGAG 1200  
 QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264  
 DB 1201 CAGCAGTACCGAAGCTGCTCAGTCCACGTGGTGTCTGGCTTGTGCCACTCTTCGGTGTCCAC 1260  
 QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284  
 DB 1261 TACACCGCTTCTATGGCTTGGCGTACACGAGGTCTCAGGAGACACTGTGGCAGATCCAG 1320  
 QY 285 MetHisTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys 304  
 DB 1321 ATGCATATCAGATGCTCTTCAACTCTCTCCAGGATTTTGTGTGCCATCATATATCTGT 1380  
 QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324  
 DB 1381 TTCTGCAATGTTGAGGTGCGAGGAGATAGGAAGTCTTGGAGCGCTGGACACTGGCA 1440  
 QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerSerTyrSerTyrGlyProMetVal 344  
 DB 1441 TTGACTTCAAGCGTAAAGCAGCAAGTGGGAGTAGCAGCTACAGCTATGCGCCCAATGGGT 1500  
 QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364  
 DB 1501 GCACACAGAGTGTGACCAATGTGGCGCGCGCGCGAGCTCAGCCTTCCCTTAGCCCC 1560  
 QY 365 ArgLeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysProGly 384  
 DB 1561 CGCTGCTTCTGCCACCACTTGGCCACTCCAGCTGCTGCCAGCGCCAGCGCGGC 1620  
 QY 385 AlaProAlaThrGluThrGluThrLeuProValThrMetAlaValProLysAspAspGly 404  
 DB 1621 GCTCCAGCATTCAGAAACGAAACATACCACTTACTATGACAGTTCACCAAGGACGAGCGC 1680  
 QY 405 PheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArgProPro 424  
 DB 1681 TTCTTAATGGCTCTGCTCGGGTCTGGATGAGAGAGCGCTCTGGGTCTGCGCGCGCCACCT 1740  
 QY 425 ProLeuLeuGlnGlyTrpGluThrValMet 435  
 DB 1741 CCATTGTTCAGAGAGAGATGGGAAACAGTCTATG 1773



















Db 421 AAAGGCCATGCTACCGACGCTGTGACCGCAATGGCAGCTGGGAGCTGGTGCTGGGCAC 480  
QY 25 ----- 25  
Db 481 AACAGGACGTGGGCCAACTACAGCGAGTGTGTCAAAATTTCTACCAATGAGACTCGTGAA 540  
QY 26 ---GluValPheAspArgLeuGlyMetIleTyrThrValGlyTyrSerMetSerLeuAla 44  
Db 541 CGGGAGGTGTTTACCGCCTGGGATGATTTACCGTGGGCTACTCCGTGTCCCTGGCG 600  
QY 45 SerLeuThrValAlaValLeuIleLeuAlaTyrPheArgArgLeuHisCysThrArgAsn 64  
Db 601 TCCCTCACCGTAGCTGTGCTCATCTGGCCTACTTTAGCGGGCTGCACGCGCGCAAC 660  
QY 65 TyrIleHisMetHisMetPheLeuSerPheMetLeuArgAlaIleSerIlePheValLys 84  
Db 661 TACATCCACATGACACCTGTTCTCTGTCTTCATGTGCGCGCGGTGAGCATCTTCGTCAAG 720  
QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGlu 104  
Db 721 GAGCGTGTCTACTCTGCGGCACGCTTGATGAGGCTGAGCGCTCACCGAGGAG 780  
QY 105 LeuHisIleIleAlaGlnValProProAlaAlaAlaAlaValAlaGlyTyrAlaGly 124  
Db 781 CTGGCGGCATCGCCAGCGCGCCCGCGCTGCCACCGCGCTGCGGCTACCGGGC 840  
QY 125 CysArgValAlaValThrPhePheLeuTyrPheLeuAlaThrAsnTyrTyrTrpIleLeu 144  
Db 841 TGCAGGGTGGCTGTGACCTTCTCTTACTTCTGCGCCACCACTACTACTGGAATCTG 900  
QY 145 ValGluGlyLeuTyrLeuHisSerLeuIlePheMetAlaPhePheSerGluLysLysTyr 164  
Db 901 GTGAGGGGCTGTACCTGCGACAGCTCATCTTCATGGCCCTTCTCTCAGAGAGAGTAC 960  
QY 165 LeuTrpGlyPheThrIlePheGlyTrpGlyLeuProAlaValPheValAlaValTrpVal 184  
Db 961 CTGTGGGGCTTCACAGTCTTCGGCTGGGGTCTGCCGCTGTCTTCGTGGGTGTGGGTC 1020  
QY 185 GlyValArgAlaThrLeuAlaAsnThrGlyCysTrpAspLeuSerSerGlyHisLysLys 204  
Db 1021 AGTGTACAGAGTACCTCGGCCAACACCGGGTGTGGGACTTGAGCTCCGGGAACAAAAAG 1080  
QY 205 TrpIleIleGlnValProIleLeuAlaSerValValLeuAsnPheIleLeuPheIleAsn 224  
Db 1081 TGGATCATCCAGGTGCCCTCCCTGGCCCTCATTTGTGTCACTTCATCTCTTCATCAAT 1140  
QY 225 IleIleArgValLeuAlaThrLysLeuArgGluThrAsnAlaGlyArgCysAspThrArg 244  
Db 1141 ATCGTCCGGTGTCTCGCCACCAAGCTCGGGAGACCAACGCGCGCGGTGTGACACACGG 1200  
QY 245 GlnGlnTyrArgLysLeuLeuArgSerThrLeuValLeuValProLeuPheGlyValHis 264  
Db 1201 CAGCAGTACCGGAGAGTGTCTCAATCCAGCTGGTGTCTATGCCCCCTCTTTGGCGTCCAC 1260  
QY 265 TyrThrValPheMetAlaLeuProTyrThrGluValSerGlyThrLeuTrpGlnIleGln 284  
Db 1261 TACATTGTCTTCATGGCCACACCATACCGAGGTCTCAGGAGCGCTCTGGCAAGTCCAG 1320  
QY 285 MethIleTyrGluMetLeuPheAsnSerPheGlnGlyPhePheValAlaIleIleTyrCys 304  
Db 1321 ATGCACATGAGATGCTCTTCAACTCTCTCCAGGGAATTTTGTGCGCAATCATATACTGT 1380  
QY 305 PheCysAsnGlyGluValGlnAlaGluIleArgLysSerTrpSerArgTrpThrLeuAla 324  
Db 1381 TTCTGCAACGCGGAGGTACAGCTGAGATCAAGAAATCTTGAGCGCGCTGGACACTGGCA 1440  
QY 325 LeuAspPheLysArgLysAlaArgSerGlySerSerTyrSerTyrGlyProMetVal 344  
Db 1441 CTGACCTTCACAGCGAAGGACCGCAGCGGAGAGAGCTATAGTACGGCCCCCATGGTG 1500  
QY 345 SerHisThrSerValThrAsnValGlyProArgAlaGlyLeuSerLeuProLeuSerPro 364  
Db 1501 TCCACACAGAGTGTGACCAATGTGCGGCCCGCGTGTGGGACTCGGCGCTGCCCTCAGCCCC 1560

QY 365 Arg---LeuProProAlaThrThrAsnGlyHisSerGlnLeuProGlyHisAlaLysPro 383  
Db 1561 CGCCTACTGCCACTGCCACCACCAACGCGCACCTCAGCTGCTGGCCATGCCAGCCA 1620  
QY 384 GlyAlaProAlaThrGluThr---GluThrLeuProValThrMetAlaValProLysAsp 402  
Db 1621 GGGACCCCGCCCTGGAGACCCTCGAGACCCACACACCACTGCCATGGCTGCTCCCAAGGAC 1680  
QY 403 AspGlyPheLeuAsnGlySerCysSerGlyLeuAspGluAlaSerGlySerAlaArg 422  
Db 1681 GATGGGTTCCTCAACGGCTCTCTCAGGCTCGAGAGAGGAGGCTTGGGCTGAGCGG 1740  
QY 423 ProProProLeuLeuGlnGluGlyTrpGluThrValMet 435  
Db 1741 CCACCTGCCCTGTCTACAGGAAGAGTGGGAGACAGTCAATG 1779

Search completed: November 24, 2004, 03:22:06

Job time : 665 secs

GenCore version 5.1.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 24, 2004, 02:13:46 ; Search time 5806 Seconds  
(without alignments)  
3543.062 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGARIAPSLALLCCPVLS.....EASGSARPPPLQGWETVM 435

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=GenEmbl -QMT=fastcap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=500 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
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Database :

GenEmbl.\*  
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2: gb\_hgt.\*  
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4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2283	100.0	1320	6	BD270931 PHT recep
2	2263.5	99.1	1335	6	BD266835 PTH funct
3	2195	96.1	2051	6	I17766 Sequence 3
4	2187	95.8	1836	10	RATPTHYR

5	2187	95.8	2065	10	RATPTHYR
6	2156	94.4	2089	10	BC051981
7	2148	94.1	2189	10	BC013446
8	2146	94.0	1984	10	MMPHRPR
9	2077.5	91.0	1363	6	BD266847
10	2077	91.0	1380	6	BD266846
11	2076.5	91.0	1380	6	BD266845
12	2008	88.0	1782	9	AY449732
13	2008	88.0	1785	6	CQ831233
14	2008	88.0	1947	6	CO714121
15	2008	88.0	1948	6	AR270690
16	2008	88.0	1948	6	AX548943
17	2008	88.0	1948	9	HMPHTR
18	2008	88.0	2095	9	HSPHR
19	2008	88.0	2171	9	HSU17418
20	2002	87.7	1782	6	AX280939
21	2002	87.7	2010	6	I17767
22	1970	86.3	1770	4	AF288463
23	1957	85.7	2177	4	AF167095
24	1932	84.6	1859	4	AY328401
25	1925	84.3	2067	4	SSU18315
26	1710	74.9	1863	6	I17765
27	1710	74.9	1878	4	OPOTHR
28	1696	74.3	975	6	BD266837
29	1687	73.9	1862	6	I17764
30	1676.5	73.4	1002	6	BD266836
31	1484	65.0	2928	6	CQ831243
32	1465	64.2	1609	6	BD249740
33	1465	64.2	1609	6	AR302320
34	1465	64.2	2129	5	AF132084
35	1395.5	61.1	23135	2	AC098311
36	1376	60.3	238330	2	AC114361
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## ALIGNMENTS

RESULT 1  
BD270931  
LOCUS BD270931 1320 bp DNA linear PAT 17-JUL-2003  
DEFINITION PHT receptor and screening assay utilizing the same.  
ACCESSION BD270931  
VERSION BD270931.1 GI:33080699  
KEYWORDS JP 2002534081-A/1.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 1320)  
AUTHORS Gardella,T.J., Kronenberg,H.M. and Jr,J.T.P.  
TITLE PHT receptor and screening assay utilizing the same  
JOURNAL Patent: JP 2002534081-A 1 15-OCT-2002;  
THE GENERAL HOSPITAL CORP  
COMMENT OS Artificial Sequence  
PN JP 2002534081-A/1  
PD 15-OCT-2002  
PF 31-DEC-1998 JP 2000592396  
PI THOMAS J GARDELLA, HENRY M KRONENBERG JOHN T POTTS JR PC  
C12N15/09,C07K14/72,C07K16/28,C12N1/15,C12N1/19,C12N1/21,C12N5/PC

10, C12P21/02,C12Q1/02,C12N15/00,C12N5/00  
CC Description of Artificial Sequence: cDNA  
FH Key Location/Qualifiers  
FT CDS (1)..(1308).  
source Location/Qualifiers  
1..1320

score: 27.3077

Alignment Scores:  
Pred. No.:  
Score:

Percent Similarity:	97.75%	Conservative:	0
Best Local Similarity:	97.75%	Mismatches:	1
Query Match:	99.15%	Indels:	9
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US-09-869-565-2 (1-435) x BD266935 (1-1335)			
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Qy	112	ProProProAlaAlaAlaValGlyTyrAlaGlyCysArgValAlaValThrPhe	131
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 DEFINITION Rat parathyroid hormone/parathyroid hormone related-peptide  
 receptor mRNA, complete cds.  
 ACCESSION LI9475.1 GI:467316  
 VERSION 1  
 KEYWORDS parathyroid hormone; parathyroid hormone receptor; parathyroid hormone-related protein; parathyroid hormone-related receptor.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 REFERENCE 1 (bases 1 to 1836)  
 AUTHORS Pausova,Z., Bourdon,J., Clayton,D., Mattei,M.G., Seidin,M.F., Janicic,N., Riviere,M., Szpirer,J., Levan,G., Szpirer,C., Goltzman,D. and Hendy,G.N.  
 TITLE Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (PTHr) cDNA from a rat osteosarcoma (UMR 106) cell line: chromosomal assignment of the gene in the human, mouse, and rat genomes  
 JOURNAL Genomics 20 (1), 20-26 (1994)  
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 PUBMED 8020952  
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/product="parathyroid hormone/parathyroid hormone  
 related-peptide receptor"

## ORIGIN

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 Percent Similarity: 73.43% Conservatives: 0  
 Best Local Similarity: 73.43% Mismatches: 1  
 Query Match: 95.80% Indels: 156  
 DB: 10 Gaps: 1

US-09-869-565-2 (1-435) x RATPTH (1-1836)

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 QY 46 ATGGGGGGCGCGGATCGCACCCAGCGCTGCTACTCTGCTGCGCCAGTGTCCAGC 105  
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 QY 21 SerAlaTyrAlaLeu----- 25  
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 QY 106 TCCGATATGCGTGGTGGATGCGGACGATGCTTTACAAAGAGAAACAGATTTCCTCG 165  
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QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGlu 104  
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RESULT 5  
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 LOCUS Rat parathyroid hormone receptor mRNA, complete cds.  
 DEFINITION M77184  
 ACCESSION  
 VERSION  
 KEYWORDS parathyroid hormone receptor; parathyroid hormone-related receptor; transmembrane glycoprotein.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 REFERENCE 1 (bases 1 to 2065)  
 AUTHORS Abou-Samra, A.-B.B., Jueppner, H., Force, T., Freeman, M.W., Kong, X.-F., Schipani, E., Urena, P., Richards, J., Bonventre, J.V., Potts, J.T., Kronenberg, H.M. and Segre, G.V.  
 TITLE Expression cloning of a common receptor for parathyroid hormone and parathyroid hormone-related peptide from rat osteoblast-like cells: a single receptor stimulates intracellular accumulation of both cAMP and inositol trisphosphates and increases intracellular free calcium  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 89 (7), 2732-2736 (1992)  
 MEDLINE 92212903  
 PUBMED 1313566  
 COMMENT Original source text: Rattus norvegicus cDNA to mRNA.  
 Complete title:  
 Expression cloning of a common receptor for parathyroid hormone and parathyroid hormone-related peptide from rat osteoblast-like cells: A single receptor stimulates intracellular accumulation of both cAMP and inositol trisphosphates and increases intracellular free calcium.

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 DEFINITION Mus musculus parathyroid hormone receptor 1, mRNA (cDNA clone MGC:62276 IMAGE:6402767), complete cds.  
 ACCESSION BC051981  
 VERSION BC051981.1 GI:30354698  
 KEYWORDS MGC.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
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 Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932  
 2 (bases 1 to 2089)  
 Strausberg, R.  
 Direct Submission  
 Submitted (01-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library Preparation: M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 114 Row: n Column: 24  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755221.

## FEATURES

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 DEFINITION M.musculus mRNA for parathyroid hormone/parathyroid hormone related peptide receptor.  
 X78936  
 ACCESSION  
 VERSION X78936.1 GI:474828  
 KEYWORDS G-protein coupled receptor; parathyroid hormone; parathyroid hormone related peptide receptor; parathyroid hormone-related hormone related peptide receptor; parathyroid hormone-related protein.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS Karperien,M., Van Dijk,T.B., Hoeijmakers,T., Cremers,F., Abou-Samra,A.B., Boonstra,J., De Laat,S.W. and Defize,L.H.K.  
 TITLE Expression pattern of parathyroid hormone/parathyroid hormone related peptide receptor mRNA in mouse postimplantation embryos indicates involvement in multiple developmental processes  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1984)  
 AUTHORS Karperien,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (21-APR-1994) M. Karperien, The Netherlands Inst. of Developmental, Biology, Uppsalalaan 8, 3584 CT Utrecht, NETHERLANDS  
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 QY 85 AspAlaValLeuTyrSerGlyPheThrLeuAspGluAlaGluArgLeuThrGluGluGlu 104  
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 novel tethered ligand-receptor molecules.  
 ACCESSION BD266847  
 VERSION BD266847.1 GI:33076615  
 KEYWORDS JP 2002533115-A/16.  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 REFERENCE 1 (bases 1 to 1363)  
 AUTHORS Gardella, F.J.; Kronenberg, H.M.; Potts, J.T. and Jueppner, H.  
 TITLE PTH functional domain conjugate peptides, derivatives thereof and  
 novel tethered ligand-receptor molecules  
 JOURNAL Patent: JP 2002533115-A 16 08-OCT-2002;  
 THE GENERAL HOSPITAL CORP  
 COMMENT OS Artificial Sequence  
 PN JP 2002533115-A/16  
 PD 08-OCT-2002  
 PF 30-DEC-1999 JP 2000591171  
 PR 31-DEC-1998 US 60/114577  
 PI THOMAS J GARDELLA, HENRY M KRONENBERG, JOHN T POTTS, HARALD PI  
 JUEPPNER  
 PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P5/18, A61P19/08, PC  
 A61P19/10,  
 PC A61P43/00, C07K14/635, C07K14/72, C07K19/00, C12N1/15, C12N1/19, PC  
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LOCUS      Homo sapiens parathyroid hormone receptor 1 (PTHRL) mRNA, complete cds.
DEFINITION      AY449732
VERSION      AY449732.1 GI:38349108
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1782)
AUTHORS      King, M.M., Aronstam, R.S. and Sharma, S.V.
TITLE      Isolation of cDNA coding for parathyroid hormone receptor 1 (PTHRL)
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 1782)
AUTHORS      King, M.M., Aronstam, R.S. and Sharma, S.V.
TITLE      Direct Submission
JOURNAL      Submitted (24-OCT-2003) Guthrie cDNA Resource Center, Guthrie Research Foundation, 1 Guthrie Square, Sayre, PA 18840, USA

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US-09-869-565-2 (1-435) x AY449732 (1-1782)

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 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
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 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
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 RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.  
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FT	CARBOHYD	161	161		N-linked (GLCNAC. . .) (Potential).
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Qy	26	-----	25
Dd	121	GAPGEVVAVCPDYIYDNFKGHAYRCDNRNGSWEVVPVGHNRTWANYSECLKFMTNETRE	180
Qy	26	-EVPDRIGMITYGVYSMSLASLTAVLILAYFRRLCHTRNYIHGMFLSPMLRAASIPVK	84
Dd	181	REVFPDRIGMITYGVYSMSLASLTAVLILAYFRRLCHTRNYIHMHMFLSPMLRAASIPVK	240
Qy	85	DAVLYSGFTTDEABRLTEEBELHIIAOVPPPPAAAAVGAGCRVAVTFFLYPLATNNYYWIL	144
Dd	241	DAVLYSGFTTDEABRLTEEBELHIIAOVPPPPAAAAVGAGCRVAVTFFLYPLATNNYYWIL	300
Qy	145	VEGIYLHSLIFMAFFSEKKYLWGFTTFGWGLPAVFVAVMVGVTRATLANTGCWLDSGGHK	204
Dd	301	VEGIYLHSLIFMAFFSEKKYLWGFTTFEGWGLPAVFVAVMVGVTRATLANTGCWLDSGGHK	360
Qy	205	WIIOVPIIASVNLNFILFINIRVLATKLRETWAGRCDTQQVRKILRSITLVLPFGVH	264
Dd	361	WIIOVPIIASVNLNFILFINIRVLATKLRETWAGRCDTQQVRKILRSITLVLPFGVH	420
Qy	265	YTTFMALPYTEVSCTLWQIQMHEMLEFNFSQGFVAIYFCNGEVOAEIRKWSRWTLA	324
Dd	421	YTTFMALPYTEVSCTLWQIQMHEMLEFNFSQGFVAIYFCNGEVOAEIRKWSRWTLA	480
Qy	325	LDFRKARKSGSSSYSGPMVSHSVTVNVGRAGLSLPLSRPLPATTTNGHSOLPGHAKPG	384
Dd	481	LDFRKARKSGSSSYSGPMGAGTSVTVNVGRAGUSLPLSRPLPATTTNGHSOLPGHAKPG	540



QY 385 APATETETLPVTWAVPKDGLNGSCGLDEEASGARPPPLQRGWETVM 435  
 DB 541 APAIENETIPVTVPDDGLNGSCGLDEEASGARPPPLQRBWETVM 591

RESULT 5  
 PTHR HUMAN  
 ID PTHR HUMAN STANDARD; PRT; 593 AA.  
 AC Q03431;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor  
 DE Precursor (PTH/PTHrP receptor) (PTH/PTHrP type I receptor).  
 GN Name-PTHr1; Synonyms-PTHr;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=93238641; PubMed=8386612;  
 RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,  
 RA Abou-Samra A.-B., Segre G.V., Jueppner H.;  
 RT "Identical complementary deoxyribonucleic acids encode a human renal  
 RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";  
 RL Endocrinology 132:2157-2165(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=93387403; PubMed=8397094;  
 RA Schneider H., Feyen J.-H., Rao Movva N.;  
 RT "Cloning and functional expression of a human parathyroid hormone  
 RT receptor.";  
 RL Eur. J. Pharmacol. 246:149-155(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95263723; PubMed=7745008;  
 RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,  
 RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,  
 RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,  
 RA Abou-Samra A.-B., Segre G.V., Jueppner H.;  
 RT "Pseudohypoparathyroidism type 1b is not caused by mutations in the  
 RT coding exons of the human parathyroid hormone (PTH)/PTH-related  
 RT peptide receptor gene.";  
 RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Levine M.A.;  
 RT "Characterization of cDNA and genomic DNA encoding the human PTH/PTHrP  
 RT receptor.";  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP EXTRACELLULAR DOMAIN DISULFIDE BONDS  
 RX MEDLINE=20374568; PubMed=10913300; DOI=10.1021/bi0001426;  
 RA Grauschopf U., Lillie H., Honold K., Wozny M., Reusch D., Esswein A.,  
 RA Schafer W., Rucknagel K.P., Rudolph R.;  
 RT "The N-terminal fragment of human parathyroid hormone receptor 1  
 RT constitutes a hormone binding domain and reveals a distinct disulfide  
 RT pattern.";  
 RL Biochemistry 39:8878-8887(2000).  
 RN [6]  
 RP STRUCTURE BY NMR OF 168-198.  
 RX MEDLINE=98409426; PubMed=9737850;  
 RA Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;  
 RA "Binding domain of human parathyroid hormone receptor: from  
 RT conformation to function.";  
 RL Biochemistry 37:12737-12743(1998).  
 RN [7]  
 RP VARIANT JMC ARG-223.

RX MEDLINE=95215874; PubMed=7701349;  
 RA Schipani E., Kruse K., Jueppner H.;  
 RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type  
 RT metaphyseal chondrodysplasia.";  
 RL Science 268:98-100(1995).  
 RN [8]  
 RP VARIANTS JMC ARG-223 AND PRO-410.  
 RX MEDLINE=96366745; PubMed=8703170;  
 RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,  
 RA Kooh S.W., Cole W.G., Jueppner H.;  
 RT "Constitutively activated receptors for parathyroid hormone and  
 RT parathyroid hormone-related peptide in Jansen's metaphyseal  
 RT chondrodysplasia.";  
 RL N. Engl. J. Med. 335:708-714(1996).  
 RN [9]  
 RP CHARACTERIZATION OF VARIANTS JMC ARG-223 AND PRO-410.  
 RX MEDLINE=97322091; PubMed=9178745;  
 RA Schipani E., Jensen G.S., Pincus J., Nissensohn R.A., Gardella T.J.,  
 RA Jueppner H.;  
 RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate  
 RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide  
 RT receptors mutated at the two loci for Jansen's metaphyseal  
 RT chondrodysplasia.";  
 RL Mol. Endocrinol. 11:851-858(1997).  
 RN [10]  
 RP VARIANT BOD LEU-132.  
 RX MEDLINE=98417978; PubMed=9745456;  
 RA Zhang P., Jobert A.-S., Couvineau A., Silve C.;  
 RT "A homozygous inactivating mutation in the parathyroid  
 RT hormone/parathyroid hormone-related peptide receptor causing  
 RT Blomstrand chondrodysplasia.";  
 RL J. Clin. Endocrinol. Metab. 83:3365-3368(1998).  
 RN [11]  
 RP VARIANT JMC ARG-458.  
 RX MEDLINE=99415605; PubMed=10487664;  
 RA Schipani E., Langman C.B., Hunzelman J., Le Merrer M., Loke K.Y.,  
 RA Dillon W.J., Silve C., Jueppner H.;  
 RT "A novel parathyroid hormone (PTH)/PTH-related peptide receptor  
 RT mutation in Jansen's metaphyseal chondrodysplasia.";  
 RL J. Clin. Endocrinol. Metab. 84:3052-3057(1999).  
 RN [12]  
 RP VARIANT ENCHONDROMATOSIS CYS-150.  
 RX MEDLINE=21918585; PubMed=11850620; DOI=10.1038/ng844;  
 RA Hopyan S., Gokgoz N., Poon R., Gensure R.C., Yu C., Cole W.G.,  
 RA Bell R.S., Jueppner H., Andrusis I.L., Wunder J.S., Alman B.A.;  
 RT "A mutant PTH/PTHrP type I receptor in enchondromatosis.";  
 RL Nat. Genet. 30:306-310(2002).  
 CC -!- FUNCTION: This is a receptor for parathyroid hormone and for  
 CC parathyroid hormone-related peptide. The activity of this receptor  
 CC is mediated by g proteins which activate adenylyl cyclase and also  
 CC a phosphatidylinositol-calcium second messenger system.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Expressed in most tissues. Most abundant in  
 CC kidney, bone and liver.  
 CC -!- DISEASE: Defects in PTHr1 are the cause of Jansen's metaphyseal  
 CC chondrodysplasia (JMC) [MIM:156400]. JMC is a rare autosomal  
 CC dominant disorder characterized by a short-limbed dwarfism  
 CC associated with hypercalcemia and normal or low serum  
 CC concentrations of the two parathyroid hormones.  
 CC -!- DISEASE: Defects in PTHr1 are the cause of chondrodysplasia  
 CC Blomstrand type (BOCD) [MIM:215045]. BOCD is a severe skeletal  
 CC dysplasia.  
 CC -!- DISEASE: Defects in PTHr1 can be a cause of enchondromatosis  
 CC [MIM:166000]. Enchondromas are common benign cartilage tumors of  
 CC bone. They can occur as solitary lesions or as multiple lesions in  
 CC enchondromatosis (Ollier and Maffucci diseases). Clinical problems  
 CC caused by enchondromas include skeletal deformity and the  
 CC potential for malignant change to osteosarcoma.  
 CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.  
 CC -----  
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CC EMBL; L04308; AAA36525.1; --
CC EMBL; X68596; CNA48589.1; --
CC EMBL; U22409; AAB60657.1; --
CC EMBL; U22401; AAB60657.1; JOINED.
CC EMBL; U22402; AAB60657.1; JOINED.
CC EMBL; U22403; AAB60657.1; JOINED.
CC EMBL; U22404; AAB60657.1; JOINED.
CC EMBL; U22405; AAB60657.1; JOINED.
CC EMBL; U22406; AAB60657.1; JOINED.
CC EMBL; U22407; AAB60657.1; JOINED.
CC EMBL; U22408; AAB60657.1; JOINED.
CC EMBL; U17418; AAA56774.1; --
CC PIR; I38139; A49191.
CC PDB; 1BL1; NMR; @=168-198
CC PDB; 1ET3; Model; S=168-469.
CC PDB; 1ET3; Model; S=168-469.
CC Genew; HGNC:9608; PTHR1.
CC MIM; 168468; --
CC MIM; 156400; --
CC MIM; 215045; --
CC MIM; 166000; --
CC GO; GO:0005737; C:cytoplasm; TAS.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005634; C:nucleus; TAS.
CC GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.
CC GO; GO:0007187; P:G-protein signaling, coupled to cyclic nucl. . .; TAS.
CC GO; GO:0001501; P:skeletal development; TAS.
CC InterPro; IPR000832; GPCR_secretin.
CC Pfam; PF00002; 7tm_2; 1.
CC Pfam; PF02793; HRM; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC SMART; SM00008; HormR; 1.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; 1.
CC PROSITE; PS00652; G_PROTEIN_RECEP_F2_4; 1.
CC PROSITE; PS00653; G_PROTEIN_RECEP_F2_5; 1.
CC 3D-structure; Disease mutation; Dwarfism; G-protein coupled receptor;
KW Glycoprotein; Signal; Transmembrane.
KW SIGNAL 1 26 Potential.
FT CHAIN 27 593 Parathyroid hormone/parathyroid hormone-
FT related peptide receptor.
FT DOMAIN 27 188 Extracellular (Potential).
FT TRANSMEM 189 212 1 (Potential).
FT TRANSMEM 213 219 Cytoplasmic (Potential).
FT TRANSMEM 220 239 2 (Potential).
FT TRANSMEM 240 282 Extracellular (Potential).
FT TRANSMEM 283 306 3 (Potential).
FT TRANSMEM 307 320 Cytoplasmic (Potential).
FT TRANSMEM 321 342 4 (Potential).
FT TRANSMEM 343 361 Extracellular (Potential).
FT TRANSMEM 362 382 5 (Potential).
FT TRANSMEM 383 409 Cytoplasmic (Potential).
FT TRANSMEM 410 428 6 (Potential).
FT TRANSMEM 429 440 Extracellular (Potential).
FT TRANSMEM 441 463 7 (Potential).
FT TRANSMEM 464 593 Cytoplasmic (Potential).
Query Match 88.0%; Score 2008; DB 1; Length 593;
Best Local Similarity 67.3%; Pred. No. 3e-143;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
DB 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAAQCEKRLKEVLQRP 60
QY 26 ----- 25
DB 61 SIMESDKGWTSGTKPRKDKASGLYPSEEDKEAPTSGRYGRPCLPEDWHILCWPL 120
QY 26 ----- 25

61 SIMESDKGWTSGTKPRKDKASGLYPSEEDKEAPTSGRYGRPCLPEDWHILCWPL 120
26 ----- 25
121 GAFGEVVAVPCPDYIYDFNHKHAYRRCDRNGSWELVPGHNRWTWYNSVCUKFLNETRE 180
26 -EVPDRGLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRYNIHMHFSLFMLRAASIFVK 84
181 REVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRYNIHMHFSLFMLRAASIFVK 240
85 DAVLYSGFTLDEAERLTEELHIIAQQPPPPAAAAGYACRVAATFFFLFELATNYWIL 144
241 DAVLYSGATLDEAERLTEELRAIAQAPPPPPATAAAGYACRVAATFFFLFELATNYWIL 300
145 VEGLYLHSLIFMAFSEKKYLWGTFTFGWGLPAVFVAVWVGVRATLANTGCDLSSGHKK 204
301 VEGLYLHSLIFMAFSEKKYLWGTFTFGWGLPAVFVAVWVGVRATLANTGCDLSSGHKK 360
205 WIIQVPIASVILNFIINIRVLATKLRNAGRCDTQOYRKLRLSTLVLPFGVH 264
361 WIIQVPIASVILNFIINIRVLATKLRNAGRCDTQOYRKLRLSTLVLPFGVH 420
265 YTVFMALPYTEVSGTLWQIOHMYEMLFNSFGFFVAILIYCFNCEVQAEIKKSWRTLA 324
421 YIVFMATPYTEVSGTLWQVQVHMYEMLFNSFGFFVAILIYCFNCEVQAEIKKSWRTLA 480
325 LDFKRSKSSSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATNGHSQLPGHAKP 383
481 LDFKRSKSSSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATNGHSQLPGHAKP 540
384 GAPATET-ETLPVTVMAVPKDDGFLNGSCGLDEEASGARPPPLLOEGWETVM 435
541 GTPALETLETPPAMAAPKDDGFLNGSCGLDEEASGARPPPLLOEGWETVM 593

RESULT 6
AAR18076 PRELIMINARY; PRT; 593 AA.
ID AAR18076
AC AAR18076;
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
GN Parathyroid hormone receptor 1.
DB PTHR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA King M.M., Atonstam R.S., Sharma S.V.;
RT "Isolation of cDNA coding for parathyroid hormone receptor 1
RT (PTHr1).";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY449732; AAR18076.1; --
KW Receptor.
SQ SEQUENCE 593 AA; 66360 MW; DA1400640A6C7F2B CRC64;
Query Match 88.0%; Score 2008; DB 2; Length 593;
Best Local Similarity 67.3%; Pred. No. 3e-143;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
DB 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAAQCEKRLKEVLQRP 60
QY 26 ----- 25
DB 61 SIMESDKGWTSGTKPRKDKASGLYPSEEDKEAPTSGRYGRPCLPEDWHILCWPL 120
QY 26 ----- 25

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Qy	1	MGARIAPSLALLCCPVLSSAYAL-----	25
Db	1	MGAVRIAPGLALLCCPVLSSAYALVDADVMTKBEQIFLLHRAQAQCQKRLKEVLQRP	60
Qy	26	-----	25
Db	61	DIMESDKCWAASASTSGKPKKPKKASGLYPESEEDKEVPTGSRHGRGPCUPEWDHILCWPL	120
Qy	26	-----	25
Db	121	GAPGEVWAVPCDYIDFNHKGHAVRRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE	180
Qy	26	-EVEDRLGMIYTVGYSMSLASLTWAVLILAYFRRRLHCTRNYYTHMFWLSFMLRAASIFVK	84
Db	181	REVEDRLGMIYTVGYSVSLASLTWAVLILAYFRRRLHCTRNYYTHMHLFLSFMLRAVSI	240
Qy	85	DAVLYSGFTLDEAERLTBEEELHIITAOVPPPPAAAAVAGVACRVAVTFPFLYFIATNYWIL	144
Db	241	DAVLYSGNTLDEAERLTBEEELRAITAOAPPPPTAAA-GVAGCRVAVTFPFLYFIATNYWIL	299
Qy	145	VEGYLHLSLIPMAFFSEKKYLGWFTIFGWGLPAVFVAWVGVRATLANTGCWDLSSGHKK	204
Db	300	VEGYLHLSLIFMAFFSEKKYLGWTFVFGWGLPAVFVAWVSVRATLANTGCWDLSSGNKK	359
Qy	205	WIIQVPIILASVVLNFIILFINIIRVLATKLRETNAGRCOTQOQYRKLIRSTVLVPLFGVH	264
Db	360	WIIQVPIILASVVLNFIILFINIIRVLATKLRETNAGRCOTQOQYRKLKSTLVLMPFLGVH	419
Qy	265	YTFVMAFPYTEVSGTLQIOHMYELMFSFGFFVAILIYFCNGEQVQAEIRKSWRWTILA	324
Db	420	YIVFMAFPYTEVSGTLQVQVQHYELMFSFGFFVAILIYFCNGEQVQAEIKKSWRWTILA	479
Qy	325	LDFFRKARSGSSSYSGYGPWMSHTSVTNVGPAGLSLPSRLPP-----ATTNGHSOL	377
Db	480	LDFFRKARSGSSSYSGYGPWMSHTSVTNVGPAGLSLPSRLPPAAATTTATTNGHPPI	539
Qy	378	PGHAKPGAPATETETLPTV---MAVPKDDGFLNGSCGLDEEASCSARPPPLLOEQWETV	434
Db	540	PGHTKPGAP-----TLPATPATAPKDDGFLNGSCGLDEEASAPERPPALLQEEWETV	594
Qy	435	M 435	
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Db	595	M 595	

RESULT #	Q7YR13	PRELIMINARY;	PRT;	589 AA.
ID	Q7YR13			
AC	Q7YR13;			
DT	01-OCT-2003	(TRENBLrel. 25, Created)		
DT	01-OCT-2003	(TRENBLrel. 25, Last sequence update)		
DT	01-MAR-2004	(TRENBLrel. 26, Last annotation update)		
DE	Parathyroid hormone/parathyroid hormone related protein receptor.			
DE	Cervus elaphus (Red deer).			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae			
OC	Cervinae; Cervus.			
OX	NCBI_TaxID=9860;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	Liu H., Barling P.M., Ma L., Nicholson L.F.B.;			
RA	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AY328401; AAP93208.1; --			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0004930; F:G-protein coupled receptor activity; IEA.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	InterPro; IPR000832; GPCR secretin.			
DR	InterPro; IPR001879; hormn_receptor.			
DR	Pfam; PF00002; 7tm_2; 1.			
DR	Pfam; PF02793; HRM; 1.			
DR	SMART; SM00008; HormR; 1.			
DR	PROSITE; PS00649; G PROTEIN RECP F2 1; 1.			

DR PROSITE; PS50227; G PROTEIN RECEPTOR F2\_3; 1.  
 DR PROSITE; PS50261; G PROTEIN RECEPTOR F2\_4; 1.  
 DR RECEPTOR.  
 SQ SEQUENCE 589 AA; 65733 MW; 08A0577F8042A77A CRC64;

Query Match 84.6%; Score 1932; DB 2; Length 589;  
 Best Local Similarity 65.2%; Pred. No. 1.6e-137;  
 Matches 386; Conservative 15; Mismatches 31; Indels 160; Gaps 4;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25  
 Db 1 MGAARIAPGLALLCCPVLSSAYALVDADDMVTKEQIFLLHRAQAQCKRLKEVLQRP 60  
 Qy 26 ----- 25  
 Db 61 DIMESDKGWASASTSGPKPKKASGKULHPESEDEKVEPTGSRGRPCLPEDWDHILCWPM 120  
 Qy 26 ----- 25  
 Db 121 GAPGEVAMPCCPDYIDFNHKGHAYRRCDNRGSMELVPGHNRWTWANYSECVKFLTNETRE 180  
 Qy 26 -EVPDRGLGMIYTVGYSYSLASLTAVLILAYFRLHCTRNVIHMHFLSFWLRAASIFVK 84  
 Db 181 REVFDRLGMIYTVGYSYSLASLTAVLILAYFRLHCTRNVIHMHFLSFWLRAASIFVK 240  
 Qy 85 DAVLYSGFTLDEARLTTEELHIIIAQVPPPPAAAGVAGCRVAVTFPLFLATNYWIL 144  
 Db 241 DAVLYSGTALDEARLTTEELHIIIAQVPPPPAAAGVAGCRVAVTFPLFLATNYWIL 299  
 Qy 145 VEGLYLSLIFMAFFSEKYLWFTIFGWLGPVAVFVAVVGVRAATLANTGWDLSGGHK 204  
 Db 300 VEGLYLSLIFMAFFSEKYLWFTIFGWLGPVAVFVAVVGVRAATLANTGWDLSGGKK 359  
 Qy 205 WIIQVPIASVNLFIPIIIRVLAATKLRTNAGRCOTQOYKRLRLSTLVLPLFGVH 264  
 Db 360 WIIQVPIASVNLFIPIIIRVLAATKLRTNAGRCOTQOYKRLRLSTLVLPLFGVH 419  
 Qy 265 YTFMALPYTEVSGTLWQIQHVMELFNSFGFPVAILIYFCNGEVOAEIKKSWRTLA 324  
 Db 420 YIVFMATPYTEVSGTLWQIQHVMELFNSFGFPVAILIYFCNGEVOAEIKKSWRTLA 479  
 Qy 325 LDFPKRKARSGSSSYSGYPMVSHTSVTNVGPRAGLSPLSPR-LPPATNGHSQLPGHAKP 383  
 Db 480 LDFPKRKARSGSSSYSGYPMVSHTSVTNVGPRAGLSPLSPR-LPPATNGHSQLPGHAKP 539  
 Qy 384 GAPATETETPLVTMAVPKDDGFLNGSCGLDEEASGSARPPILQEGWETVM 435  
 Db 540 GSPA--LQATPPAFAAPKEDGFLNGSCGLDEEACAPERPVLQEGWETVM 589

RESULT 9  
 PTRR\_PIG STANDARD; PRT; 585 AA.  
 ID PTRR\_PIG AC PS0133;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Parathyroid hormone/parathyroid hormone-related peptide receptor  
 DE Precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).  
 GN Name=PTHRI; Synonyms=PTHRI;  
 OS Sus scrofa (pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=96305358; PubMed=8688470;  
 RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,  
 RA Chandrasekhar S., Heising H.M.;  
 RT "Structure and functional expression of a complementary DNA for  
 RT porcine parathyroid hormone/parathyroid hormone-related peptide  
 RT receptor";  
 RL Biochim. Biophys. Acta 1307:339-347(1996).

-1- FUNCTION: This is a receptor for parathyroid hormone and for parathyroid hormone-related peptide. The activity of this receptor is mediated by G proteins which activate adenyl cyclase and also a phosphatidylinositol-calcium second messenger system (By similarity).  
 -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 -1- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.  
 -----  
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 CC EMBL; U08315; AAC48619.1; --  
 CC HSP; Q03431; IBL1.  
 CC InterPro; IPR000832; GPCR secretin.  
 CC InterPro; IPR001879; hormn\_receptor.  
 CC Pfam; PF00002; 7tm.2; 1.  
 CC Pfam; PF02793; HRM\_1.  
 CC PRINTS; PR00249; GPCRSECRETIN.  
 CC SMART; SM00008; Hormr; 1.  
 CC PROSITE; PS00649; G PROTEIN RECEPTOR F2\_1; 1.  
 CC PROSITE; PS00650; G PROTEIN RECEPTOR F2\_2; 1.  
 CC PROSITE; PS00227; G PROTEIN RECEPTOR F2\_3; 1.  
 CC PROSITE; PS00261; G PROTEIN RECEPTOR F2\_4; 1.  
 CC G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.  
 KW SIGNAL 1 26  
 FT FT 27 585  
 CHAIN  
 FT DOMAIN 27 184  
 FT TRANSMEM 185 208  
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 FT TRANSMEM 216 235  
 FT DOMAIN 236 277  
 FT TRANSMEM 278 301  
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 FT DOMAIN 424 435  
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 FT DOMAIN 459 585  
 FT DISULFID 48 113  
 FT DISULFID 104 144  
 FT DISULFID 127 166  
 FT CARBOHYD 147 147  
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 FT CARBOHYD 162 162  
 FT CARBOHYD 172 172  
 SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;

Query Match 84.3%; Score 1925; DB 1; Length 585;  
 Best Local Similarity 65.6%; Pred. No. 5.5e-137;  
 Matches 386; Conservative 13; Mismatches 33; Indels 156; Gaps 4;

Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25  
 Db 1 MGAARIAPGLALLCCPVLSSAYALVDADDMVTKEQIFLLHRAQAQCKRLKEVLQRP 60  
 Qy 26 ----- 25  
 Db 61 DIMESDKGWASAPTSGPKPKKASGKLYPESGEDTGSRHQGRPCLPEDWDHILCWPLGAP 120  
 Qy 26 ----- 28  
 Db 121 EVVAMPCEDIYDFNHHKGHAYRRCDNRGSMELVPGHNRWTWANYSECVKFLTNETREVF 180  
 Qy 29 DRLGMIYTVGYSYSLASLTAVLILAYFRLHCTRNVIHMHFLSFWLRAASIFVKDAVL 88

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Db 181 DR LGMVTVGVSVSLASLTAVLILAYFRRLHCTRNIIHMLFLSMLRAVSIFVKDAVL 240
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Db 241 YSGATLDEARLTEREELRAIAQAPLPP-VAATSYGCRVAVTFYFLATNYYWILVEGL 299
QY 149 YLHSLIFMAFFSEKKYLWGFTIFGWLPAFVAVVWVVRATLANTCGDLSGSKWIIQ 208
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QY 209 VPILASVNLNFIINIRVLATKLRETNAGRCDTROQVRKLLRSTLVLPVLFVGHYTP 268
Db 360 VPILASVNLNFIINIRVLATKLRETNAGRCDTROQVRKLLRSTLVLPVLFVGHYTP 419
QY 269 MALPTEVSGTLWQIQOMHYEMLFNSFGQFFVAIYFCNGEVOAEIRKSWRWTLLALDFK 328
Db 420 MATPYTEVSGTLWQIQOMHYEMLFNSFGQFFVAIYFCNGEVOAEIRKSWRWTLLALDFK 479
QY 329 RKARSGSSSYSGPMVSHSTVTVNGPRAGLSIPLSPR-LPPATTNGHSOLPGHAKGAPA 387
Db 480 RKARSGSSSYSGPMVSHSTVTVNGPRAGLSIPLSPR-LPPATTNGHSOLPGHAKGAPA 539
QY 388 TETETLPVTMAVPKDDGFLNGSCGLDERASGSRPPPLLOEGWETVM 435
Db 540 --LQTPPVWAAPKDDGFLNGSCGLDERASGSRPPPLLOEGWETVM 585

RESULT 10
PTRR DIDMA STANDARD; PRT; 585 AA.
AC P25107;
DT 01-MAY-1992 (Rel. 22, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Parathyroid hormone/parathyroid hormone-related peptide receptor
DE precursor (PTH/PTHr receptor) (PTH/PTHr type I receptor).
GN Name=PTHr; Synonyms=PTHr;
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92054592; PubMed=1658941;
RA Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani E.,
RA Richards J., Kolarowski L.F. Jr., Hock J., Potts J.T. Jr.,
RA Kronenberg H.M., Segre G.V.;
RT "A G protein-linked receptor for parathyroid hormone and parathyroid
RT hormone-related peptide."
RL Science 254:1024-1026(1991).
CC -!- FUNCTION: This is a receptor for parathyroid hormone and for
CC parathyroid hormone-related peptide. The activity of this receptor
CC is mediated by g proteins which activate adenyl cyclase and also
CC a phosphatidylinositol-calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M74445; AAA30979.1; -.
DR PIR; A39286; A39286.
DR HSSP; Q03431; 1BL1.
DR InterPro; IPR000832; GPCR_secretin.
DR InterPro; IPR001879; hormn_receptor.
DR Pfam; PF00002; 7tm.2; 1.
DR Pfam; PF02793; HRM; 1.

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DR PROSITE; PS01027; G_PROTE
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DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tatemuni S., Aburatani H., Asai K., Akiyama Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AB065462; BAC05721.1; -.
DR HSP; Q03431; IBL1.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0004930; F: G-protein coupled receptor activity; IEA.
DR GO; GO:0004991; F: parathyroid hormone receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002170; Phrmn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00393; PTRHORMONER.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00261; G_PROTEIN_RECEP_F2_4; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 964 AA; 105705 MW; 8EA72B44244DFD5D CRC64;

Query Match 74.4%; Score 1698; DB 2; Length 964;
Best Local Similarity 59.9%; Pred. No. 1.4e-119;
Matches 356; Conservative 11; Mismatches 31; Indels 196; Gaps 9;

QY 26 EVDFRLGMIYTVGYSMISLASITVAVLILAYFRNAGRGERRDMVEGGRWPRSDATPSLHP 376
DB 317 EVDFRLGMIYTVGYSMISLASITVAVLILAYFRNAGRGERRDMVEGGRWPRSDATPSLHP 376

QY 57 -----RLHCTRNTHMFLSFMLRAASIF 82
DB 377 SPAGVTVYGAQPSFLSTHRASPCPHRSCAPRRRLHCTRNTHMFLSFMLRAASIF 436

QY 83 VKDAVLSGFTLDEAERLTEELHIIAQVPPPPAAAAVGVAG----- 124
DB 437 VKDAVLSGATLDEAERLTEELRAIAQAPPPATAAGVYSTPLPARSRCHWPRGAPP 496

QY 125 -----CR----- 126
DB 497 RPAPARSPCPPPASATGFSHNSPSYVRPNPQLCRPPCCQGLRVSHPTPRAAIKAPTSTQ 556

QY 127 VAVTFYFLATNYWTLVEGLYLSLIFMAFFSEKKYLMGFTTFGWLPAVFAVAVVGV 186
DB 557 VAVTFYFLATNYWTLVEGLYLSLIFMAFFSEKKYLMGFTTFGWLPAVFAVAVVGV 616

QY 187 RATLANTGCWDLSSGHKKWIIQVPLASV--LNFILFINIRVLATKLRETNAGRCDDR 244
DB 617 RATLANTG-----VQPPDAAPSLPQLNFILFINIRVLATKLRETNAGRCDDR 664

QY 245 QOY-----RKLLRSTLVLPFGVHYTFMALPYTEVSGTLWQIQHMYEML 290
DB 665 QOYRSGALTYLPRWRPKLLKSTLVLPFGVHYTFMALPYTEVSGTLWQIQHMYEML 724

QY 291 FNSF-----QGFVFIYFCNGEVOAEIRKSWRWTL 323
DB 725 FNSFQVRSAGPLAEGGSGGRDPDRHPSGGFFVFIYFCNGEVOAEIRKSWRWTL 784

QY 324 ALDPKARKSSSSSYSGPMVSHTSVTNVPAGLSLPLSPR-LPPATTNGHSQLPGHAK 382
DB 785 ALDPKARKSSSSSYSGPMVSHTSVTNVPAGLSLPLSPRLLPTATTNGHPQLPGHAK 844

QY 383 PGAPATET-ETLPTVMVPKDDGFLNGSCSLGDEASGSRPPLPQSGWETVM 435
DB 845 FGTPALETLETTTPPAMAPKDDGFLNGSCSLGDEASGSRPPLPQSGWETVI 898

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RESULT 12
Q9PVD3 PRELIMINARY; PRT; 536 AA.
ID Q9PVD3
AC Q9PVD3
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Parathyroid hormone receptor PTHLR.
GN Name: pthrl;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99428481; PubMed=10497171;
RA Rubin D.A., Juppner H.;
RT "Zebrafish express the common parathyroid hormone/parathyroid hormone-
RT related peptide receptor (PTH1R) and a novel receptor (PTH3R) that is
RT preferentially activated by mammalian and fugu fish parathyroid
RT hormone-related peptide."
RL J. Biol. Chem. 274:28185-28190 (1999).
RE EMBL; AF132084; AAF01265.1; -.
DR HSP; Q03431; IBL1.
DR ZFIN; ZDB-GENE-991123-8; pthrl.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0004930; F: G-protein coupled receptor activity; IEA.
DR GO; GO:0004991; F: parathyroid hormone receptor activity; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR InterPro; IPR000832; GPCR secretin.
DR InterPro; IPR001879; hormn_receptor.
DR InterPro; IPR002170; Phrmn_receptor.
DR Pfam; PF00002; 7tm_2; 1.
DR Pfam; PF02793; HRM; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTRHORMONER.
DR SMART; SM00008; Hoimr; 1.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
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KW Receptor.
SQ SEQUENCE 536 AA; 61454 MW; 653B0A56DB2C8FA9 CRC64;

Query Match 64.2%; Score 1465; DB 2; Length 536;
Best Local Similarity 68.8%; Pred. No. 2.8e-102;
Matches 284; Conservative 45; Mismatches 66; Indels 18; Gaps 4;

QY 26 EVDFRLGMIYTVGYSMISLASITVAVLILAYFRRLHCTRNTHMFLSFMLRAASIFVKD 85
DB 139 EVDFRLYLYTVGYSLISLSGLMWATVILGYFRRLHCTRNTHMFLSFMLRAISIFVKD 198

QY 86 AVLYSGFTLDEAERLTEELHIIAQVPPPPAAAAVGVAGRVAVTFYFLATNYWTLV 145
DB 199 VVLYSGSALQEMERITVEDLKSITEAPP---ANKTFIGCKVAVTFYFLATNYWTLV 255

QY 146 EGLYLSLIFMAFFSEKKYLMGFTTFGWLPAVFAVAVVGVRAVLANTGCWDLSSGHKKW 205
DB 256 EGLYLSLIFMTFFSDRKYLMGFTTFGWLPAVFAVAVVGVRAVLANTGCWDLSSGHKKW 315

QY 206 IIVQPIILASVVLNFIINIRVLATKLRETNAGRCDDRQYRKLKSTLVLPFGVHY 265
DB 316 IIVQPIILTAIVNFIINIRVLATKLRETNAGRCDDRQYRKLKSTLVLPFGVHY 375

QY 266 TVFMALPYTEVSGTLWQIQHMYEMLFNSFGQFFVFIYFCNGEVOAEIRKSWRWTLAL 325
DB 376 IVFMALPYTEVSGTLWQIQHMYEMLFNSVQGFVFIYFCNGEVOAEIRKSWRWTLAL 435

QY 326 DFPRKARKSSSSSYSGPMVSHTSVTNVPAGLSLPLSPRPPATTNGHSQLPGHAKPGA 385
DB 436 DFPRKARKSSNTSYSGPMVSHTSVTNVPAGLSLPLSPRPPATTNGHSQLPGHAKPGA 495

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Db 406 FVGMPTHT-PBGLGWEERWYCELPFNFSQGFVFSIIYCYNGEYQTEIKTKTWRNLAFDW 464

Qy 328 KXKARSGSSYSYGPV-----SHTSVTVNGPRAGLSLPSRLPPA-----TTNGHS 375

Db 465 KGPVVCSSN-RYGSVLTLGLNNSTSSQSLAAGGPGTRSTTLFSSRYRSGGPTVSTHA 522

Qy 376 QLPCHAKPGAPATETPLVTMAVPKDGFLNGSCSLDE--EASGSARPPPLQSGWE 432

Db 523 TLPFGVL-----NSDADSLPPSPEEPD-----SAKQVDDILLKESLTPRPSGLEDDEE 573

Qy 433 TV 434

Db 574 TL 575

RESULT 15

ID\_PTH2\_HUMAN STANDARD; PRT; 550 AA.

AC P49150; Q8N429;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Parathyroid hormone receptor precursor (PTH2 receptor).

GN Name=PTH2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

[1]

SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RP TISSUE=Brain;

RX MEDLINE=95318121; PubMed=7797535;

RA Usdin T.B., Gruber C., Bonner T.I.;

RA "Identification and functional expression of a receptor selectively recognizing parathyroid hormone, the PTH2 receptor.";

RL J. Biol. Chem. 270:15455-15458(1995).

[2]

SEQUENCE FROM N.A.

RP TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3]

SEQUENCE OF 26-40 AND 306-550 FROM N.A.

RX MEDLINE=97079671; PubMed=8921382;

RA Usdin T.B., Modi W., Bonner T.I.;

RA "Assignment of the human PTH2 receptor gene (PTH2R) to chromosome 2q33 by fluorescence in situ hybridization.";

RL Genomics 37:140-141(1996).

CC -!- FUNCTION: This is a specific receptor for parathyroid hormone. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase.

CC -!- TISSUE SPECIFICITY: Expressed abundantly in brain and pancreas.

CC Also expressed in the testis.

CC -!- SIMILARITY: Belongs to family 2 of G-protein coupled receptors.

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DR EMBL; U25128; AAC50157.1; -

DR EMBL; BC036811; AAH36811.2; -

DR EMBL; U47124; AAA96796.1; -

DR EMBL; U47129; AAC50767.1; -

DR EMBL; U47125; AAC50767.1; JOINED.

DR EMBL; U47126; AAC50767.1; JOINED.

DR EMBL; U47127; AAC50767.1; JOINED.

DR EMBL; U47128; AAC50767.1; JOINED.

DR PIR; A57519; A57513.

DR Genew; HGNC:9609; PTHR2.

DR MIM; 601469; -

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004991; P:parathyroid hormone receptor activity; TAS.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.

DR InterPro; IPR000832; GPCR\_secretin.

DR InterPro; IPR001879; hormn\_receptor.

DR Pfam; PF00002; 7tm.2; 1.

DR Pfam; PF02793; HRM\_1

DR PRINTS; PR00249; GPCRSECRETIN.

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DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_280; 1.

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DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_294; 1.

DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_295; 1.

DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_296; 1.

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DR PROSITE; PS00650; G\_PROTEIN\_RECEP\_F2\_298; 1.

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DR PROSITE; PS0065



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Qy 201 GHKKWIIQVILASVVLNFIILFIIIRVLATKLRITNAGRCDTROQYRKLLRSTLVLVPL 260
Db 312 GDIKWIYQAPILAAIGLNFILFINTVRVLATKIWETNAVGHDTROQYRKLAKSTLVLVLV 371
Qy 261 FGVHYTFMALPYTEVSGTLWQIOMHYEMLFNSFOGFFVAILIYCFNGEVOAEIRKWSR 320
Db 372 FGVHYIVFVCLPHS-FTGLGWEIRMHCELFNSFOGFFVSIICYCNGEVOAEVKKWSR 430
Qy 321 WTLALDFRKARSGS-----SSYSYGPMSVSHTSVTNVGPRAGLSLPLSPRLPP 368
Db 431 WNLSDVWKRTPPCGSRRRCGSLTTVTHSTSSQSQVAASTRMVLI---SGKAAKIASROP- 486
Qy 369 ATTNGHSOLPGHAKPGAPATETETLP 394
Db 487 ---DSHITLPGYVWSN----SEQDCLP 506
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Search completed: November 23, 2004, 20:59:09  
Job time : 81 secs

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GenCore version 5.1.6  
Copyright (C) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 20:51:19 ; Search time 20 Seconds  
(without alignments)  
2092.715 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGARPPPLQEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2187	95.8	591	2 I54195	parathyroid hormon
2	2146	94.0	591	2 S44203	parathyroid hormon
3	2134	93.5	589	2 I59297	parathyroid hormon
4	2008	88.0	593	2 A49191	parathyroid hormon
5	1710	74.9	585	2 A39286	parathyroid hormon
6	1050.5	46.0	550	2 A57519	parathyroid hormon
7	772	33.8	459	2 JH0594	parathyroid hormon
8	757.5	33.2	449	2 S16319	vasoactive intesti
9	745	32.6	440	2 J62332	secretin receptor
10	741	32.5	460	2 J62194	secretin receptor
11	741	32.5	460	2 J62194	vasoactive intesti
12	687	30.1	525	2 JN0902	vasoactive intesti
13	684	30.0	467	2 JN0616	pituitary adenylat
14	676.5	29.6	437	2 JN0185	pituitary adenylat
15	672.5	29.5	437	2 S39069	PACAP/VIP receptor
16	671	29.4	381	2 S33449	vasoactive intesti
17	671	29.4	495	2 S39061	pituitary adenylat
18	671	29.4	495	2 S36114	pituitary adenylat
19	666	29.2	438	2 G02822	vasoactive intesti
20	666	29.2	513	2 S47631	pituitary adenylat
21	657	28.8	523	2 S39060	pituitary adenylat
22	649	28.4	462	2 J23462	gastric inhibitory
23	634.5	27.8	466	2 G02234	gastric inhibitory
24	634.5	27.8	466	2 S66676	glucose-dependent
25	613.5	26.9	455	2 I33273	glucose-dependent
26	604	26.5	463	2 A46172	glucagon-like pept
27	597.5	26.2	491	2 I37411	glucagon receptor
28	595.5	26.1	485	2 JQ1957	glucagon-like pept
29	594	26.0	463	2 S71624	glucagon-like pept

30	592	25.9	463	2 I84494	glucagon-like pept
31	582.5	25.5	485	2 JC4363	glucagon receptor
32	571.5	25.0	477	2 JC2041	glucagon receptor
33	567.5	24.9	423	2 A45363	somatoliberein rece
34	567.5	24.9	451	2 I45586	growth hormone-rel
35	560.5	24.6	423	2 S29753	growth hormone-rel
36	535	23.4	464	2 S29754	growth hormone-rel
37	521	22.8	515	2 I60800	calcitonin recepto
38	518	22.7	479	2 S33746	calcitonin recepto
39	514.5	22.5	515	2 I49154	calcitonin recepto
40	512	22.4	474	2 I37217	calcitonin recepto
41	511.5	22.4	478	2 A37430	calcitonin recepto
42	497	21.8	490	2 S34486	calcitonin recepto
43	488	21.4	482	2 A39285	calcitonin recepto
44	476	20.8	461	2 JC2477	calcitonin recepto
45	476	20.8	498	2 I47130	calcitonin recepto

#### ALIGNMENTS

##### RESULT 1

I54195

parathyroid hormone/parathyroid hormone related-peptide receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004

C:Accession: I54195; A42698

R:Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier Genomics 20, 20-26, 1994

A>Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor ( and rat genomes.

A:Reference number: I54195; MUID:94292182; PMID:8020952

A:Accession: I54195

A>Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-591 <RES>

A:Cross-references: UNIPROT:P25961; GB:I19475; NID:9467316; PIDN:AAA68098.1; PID:9467317 R:Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992

A>Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid n of both cAMP and inositol triphosphates and increases intracellular free calcium.

A:Reference number: A42698; MUID:92212903; PMID:1313566

A:Accession: A42698

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-585,'G',587-591 <ABO>

A:Experimental source: ROS 17/2.8 osteosarcoma cells

A>Note: sequence extracted from NCBI backbone (NCBIP:92187)

C:Superfamily: glucagon receptor

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Best Local Similarity	73.4%	Pred. No. 3.4e-174;		
Matches 434;	Conservative	0;	Mismatches 1;	Indels 156; Gaps 1;
QY	1	MGAARIAPSLALLCCPVLSAYAL	-----	25
Db	1	MGAARIAPSLALLCCPVLSAYALVDADVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA	60	
QY	26	-----	25	
Db	61	NIMESDKGWTASTSGKPRKEKASGKFPESKENNDVPTGSRGRPCLPEDWNVWPL	120	
QY	26	-----	25	
Db	121	GAPGEVAVPCPDYIDFNHKGHAYRCDRNGSWEVPGHNRTWANYSECLKFMNTRTE	180	
QY	26	-EVFDRLGIMYTVGYSMSLASLTAVLILAYFRLLHCTRTNYIHMHMFLSFMRLAASIFVK	84	
Db	181	REVFDRLGIMYTVGYSMSLASLTAVLILAYFRLLHCTRTNYIHMHMFLSFMRLAASIFVK	240	
QY	85	DAVLVSFTLDEAEELTEELHIIAQVPPPPAAAAGVAGCRVATFFLYFLATNYWIL	144	
Db	241	DAVLVSFTLDEAEELTEELHIIAQVPPPPAAAAGVAGCRVATFFLYFLATNYWIL	300	



539 APAIENETIPVTMTVPKDDGFLNGSCGLDEEASGSARPPPLLOEFWETVM 589

## RESULT 4

A49191  
parathyroid hormone/PTH-related peptide receptor - human  
N/Alternate names: parathyroid hormone/parathyroid peptide receptor  
C/Species: Homo sapiens (man)  
C/Date: 19-Dec-1993 #sequence revision 18-Nov-1994 #text\_change 09-Jul-2004  
C/Accession: I38139; A49191; I38113; G01562; S29610  
R/Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhmann, M.; Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.  
J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995  
A/Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons  
A/Reference number: I38139; MUID:95263723; PMID:7745008  
A/Accession: I38139  
A/Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-593 <RES>  
A/Cross-references: UNIPROT:Q03431; EMBL:U02409; NID:9897594; PIDN:AA860657.1; PID:g8975  
R/Schipani, E.; Karga, H.; Karapilis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.  
Endocrinology 132, 2157-2165, 1993  
A/Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa  
A/Reference number: A49191; MUID:93238641; PMID:8386612  
A/Accession: A49191  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-593 <SCH>  
A/Cross-references: GB:L04308; NID:gl90721; PIDN:AAA36525.1; PID:gl90722  
A/Note: sequence extracted from NCBI backbone (NCBIN:I30233, NCBIP:I30234)  
R/Schneider, H.; Feyen, J.H.; Seuwen, K.; Movva, N.R.  
Eur. J. Pharmacol. 246, 149-155, 1993  
A/Title: Cloning and functional expression of a human parathyroid hormone receptor.

A;Reference number: 138113; MUID:9338/403; PMID:8397094  
A;Accession: 138113  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-593 <RE2>  
A;Cross-references: EMBL:X68596; NID:g356812; PIDN:CAA48589.1; PID:g396813  
R;Levine, M.  
submitted to the EMBL Data Library, November 1994  
A;Reference number: G07787  
A;Accession: G01562  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-593 <LEV>  
A;Cross-references: EMBL:U17418; NID:g596129; PIDN:AAA56774.1; PID:g596130  
C;Genetics: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 45  
C;Superfamily: glucagon receptor  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 88.0%; Score 2008; DB 2; Length 593;  
Best Local Similarity 67.3%; Pred. No. 2.8e-159;  
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY 1 MGAARIAPSIALLICCPVLSAYAL----- 25

1 MGTARIAPGLALLCCPVLSSAYALVDADDVNTKEEQIFLLHRAQACEKRLKEVLORPA 60

61 SIMESDKGWTSASTSCCKPRKDKASGLYPESEEDKEAPTGSRYGRPCLPEDWHILCWPL 120

Qy 26 ----- 25

121 GAPEVVAVPCPDYIDYFNHKGHAYRCDRNSWELVPGNRTWANYSECUKELTNRE 180

20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050

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Db	241	DAVLVS	GATLDE	AEERL	TEELRA	IAQAQ	PPPPATA	AGYAC	RVAVTF	FLATN	YWIL	300				
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Db	301	VEGLY	LHSLI	FMAP	SEKKY	LMGFT	VPQ	WGLPA	VFVVM	VGVVR	ATLANT	GCWDL	SSGNKK	360		
Qy	205	WIIQV	PILAS	VVLNF	ILFIN	IRVLAT	KLRE	TNAG	RCDT	ROQYR	KLRL	STLVL	VPLFGVH	264		
Db	361	WIIQV	PILAS	VVLNF	ILFIN	IRVLAT	KLRE	TNAG	RCDT	ROQYR	KLRL	STLVL	VPLFGVH	420		
Qy	265	YTFM	ALPYT	VS	GTLM	QIOM	HYE	MLFNS	FQGF	FAI	IYFC	NGE	VQAEIR	KSWSR	WTILA	324
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Qy	325	LDFKR	KARSG	SSSYG	SGPM	VSHTS	VTNV	PRAGL	SLPL	SPR	LPP	ATTN	GH	SOLP	GHAKP	383
Db	481	LDFKR	KARSG	SSSYG	SGPM	VSHTS	VTNV	PRVGL	GLPL	SPRLL	PTATT	NGH	POLP	GHAKP		540
Qy	384	GAPAT	ET	FLPVT	MAV	PKDD	GFLNG	SCSG	GLDE	EASG	SARPP	PLP	QEG	WETVM	435	
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RESULT 5  
A39286  
parathyroid hormone / parathyroid hormone-related peptide - North American opossum  
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American  
C;Date: 24-Jan-1992 #sequence revision 24-Jan-1992 #text chang09-Jul-2004

## RESULT 5

A39286

parathyroid hormone / parathyroid hormone-related peptide - North American opossum  
C:Species: *Didelphis virginiana*, *Didelphis marsupialis virginiana* (North American opossum  
C:Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 09-Jul-2004  
C:Accession: A39286  
R:Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.; K  
Science 254, 1024-1026, 1991  
A:title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-rel.  
A:reference number: A39286; MUID:92054592; PMID:1658941  
A:Accession: A39286  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-585 <JUE>  
A:Cross-references: UNIPROT:P25107; GB:M74445  
S:Superfamily: Glucagon receptor  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 74.9%; Score 1710; DB 2; Length 585;  
Best Local Similarity 80.2%; Pred. No. 1.8e-134;  
Matches 333; Conservative 27; Mismatches 43; Indels 13; Gaps 7;

QY 26 EVEDRLGMIYTVGVSMGLASITVAVLILAYFRRLHCTRNYIHMHMFLSFMLRAASTFVKD 85

Db 179 EVDFRLGNIYTVGVSIISLGSLTVAVLILGYFRRLLCTRNYYIMHILFVSPMLRAVSIFIKD 238

[illegible]

QY 146 EGIYHLSPWAFSEKKYLVGFTIFCGGLPAVFVWVWGYRATLANTGCWDLSSCHKW 205

Db 296 EGIYLSLIPMAFFSEKKYLGWFTLFGWGLPAVFVAVVTVRATLANTECDWLSGNKKW 355

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Db 416 IVFMATPYTEVSGILMQVQVHYEMLFNSFGQFFVALLYCFNGEVOAEIKKSWSRWTLAL 475

326 DFKKKKQSSSTISIGFMWSHLSVNVGPRAGTSLFUSFRUFP---ATINGHSQUPGHAK 382  
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476 DFKRKARSGSSTYSYGMVMSHTSVTNVGPRGLALSIPRLAPGAGASGHHQLPGYYK 535

383 PGAPATETETLPYTMVPP--KDDGFLNGSCGLDEEASGSARPPPLLOEGNETVM 435

Db 536 HG--SISNSLPSGPEPGTKDDGYLNG--SGLYEPMVGE-QPPPLLEERTVM 585

RESULT 6  
A57519  
parathyroid hormone receptor 2 precursor - human  
N;Alternate names: PTH2 receptor  
C;Species: Homo sapiens (man)  
C;Date: 08-Dec-1995 #sequence\_revision 08-Dec-1995 #text\_change 09-Jul-2004  
C;Accession: A57519  
R;Usdin, T.B.; Gruber, C.; Bonner, T.I.  
J. Biol. Chem. 270, 15455-15458, 1995  
A;Title: Identification and functional expression of a receptor selectively recognizing  
A;Reference number: A57519; MUID:95318121; PMID:7797535  
A;Accession: A57519  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-550 <USD>  
A;Cross-references: UNIPROT:P49190; GB:U251128; NID:g887966; PIDN:AAC50157.1; PID:g887967  
C;Genetic:  
A;Gene: GDB:PTH22; PTHR2R  
A;Cross-references: GDB:731977; OMIM:601469  
A;Map position: 2q33-2q33  
C;Superfamily: glucagon receptor  
C;Keywords: hormone receptor

Query Match 46.0%; Score 1050.5; DB 2; Length 550;  
Best Local Similarity 53.9%; Pred. No. 1.4e-79;  
Matches 208; Conservative 58; Mismatches 85; Indels 35; Gaps 7;

Qy 26 EVFDRGMIVTVGVSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSEFMLRAASIFVKD 85  
Db 139 EFERLVMTVTVGVISFGSLAVAILIGYFRRLHCTRNVIHMHMFLSFVFLRATSIKVD 198  
Qy 86 AVLYSGFTLDEARLTEELHIIAQVPPPPAAAAGV-----YAGCRVAVTFVFLATNY 140  
Db 199 RVVHAHGVKELES-----IMQDDPQNSIBATSDVKSQYICKIAVVMFVFLATNY 251  
Qy 141 YWILVEGLYHLSLIFMAFFSEKKYLWGTFTFGWGLPAVFVAVVGVVTRATLANTCCWDLSS 200  
Db 252 YWILVEGLYHNLIFVAFSDTKYLGWFGFPAFVAVVAVARATLADARCNELSA 311  
Qy 201 GHKKWIIQVILASVNLFINIIRVLATKLRETNAGRCDTROQYRKLRLSLVLVPL 260  
Db 312 GDIKWIIQVAILAIGLNFILNTVRLATKIWETNAVGHDRKQYRKLAKSLVLVLV 371  
Qy 261 FGVHYTVFMAIPYTEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSR 320  
Db 372 FGVHYIVFVCLPHS-FTGLGWEIRMHCELPFNSFGQFFVSIYCYCNGEVOAEVKKWSR 430  
Qy 321 WTALDFKRRKSGS-----SSYSYGMVMSHTSVTVNGPRAGLSPLSPRLPP 368  
Db 431 WNLSDVWKRTFPCGSRGCVLTVTHSTSSQSQVAASRMLVLI---SGRAAKIASRQP- 486  
Qy 369 ATTNHGSQLPCHAKPGAPATETELP 394  
Db 487 ---DSHTILPGYWSN---SEQDCLP 506

RESULT 7  
JH0594  
vasoactive intestinal peptide receptor precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C;Accession: JH0594; S56014  
R;Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.  
Neuron 8, 811-819, 1992  
A;Title: Functional expression and tissue distribution of a novel receptor for vasoactive  
A;Reference number: JH0594; MUID:92232309; PMID:1314625  
A;Accession: JH0594  
A;Molecule type: mRNA  
A;Residues: 1-459 <ISH>  
A;Cross-references: UNIPROT:P30083; GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641  
A;Experimental source: lung

R;Pei, L.; Melmed, S.  
Biochem. J. 308, 719-723, 1995  
A;Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene 5'  
A;Reference number: S56014; MUID:97104266; PMID:8948424  
A;Accession: S56014  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-26 <PEI>  
A;Cross-references: EMBL:U10635; NID:g505752; PIDN:AAB48185.1; PID:g514311  
C;Superfamily: glucagon receptor  
C;Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protein  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>  
F;146-168/Domain: transmembrane #status predicted <TM1>  
F;176-195/Domain: transmembrane #status predicted <TM2>  
F;218-241/Domain: transmembrane #status predicted <TM3>  
F;256-277/Domain: transmembrane #status predicted <TM4>  
F;295-318/Domain: transmembrane #status predicted <TM5>  
F;344-363/Domain: transmembrane #status predicted <TM6>  
F;376-395/Domain: transmembrane #status predicted <TM7>  
F;58,69,100,292/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 33.8%; Score 772; DB 2; Length 459;  
Best Local Similarity 44.8%; Pred. No. 1.7e-56;  
Matches 147; Conservative 64; Mismatches 83; Indels 34; Gaps 7;

Qy 35 YTVGVSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSEFMLRAASIFVKDVLVSGFTL 94  
Db 147 YTVGVSMASLITVAVLILAYFRRLHCTRNVIHMHMFLSEFMLRAASIFVKDVLVSGFTL 206  
Qy 95 DEARLTEELHIIAQVPPPPAAAAGVAGCRVAVTFVFLATNYWILVEGLYHLSL 154  
Db 207 DHCEAS-----VCKAAVFFQYCVANFVFLVVEGLYHLSL 245  
Qy 155 FMAFFSEKKYLWGTFTFGWGLPAVFVAVVGVVTRATLANTCCWD-LSSGHKKWIIQVPLA 213  
Db 246 AVSFFSEKKYFVGWGLVGVVPSVFTITVTVRIYFEDFGWDTIINSSLLWIIKAPILL 305  
Qy 214 SVVNLFIINIRVLATKLRETNAGRCDTROQYRKLRLSLVLVPLFGVHYTVFMAIPY 273  
Db 306 SILVNFVLFICIRILVQKLRPPDIGNKDS-SPYSRLAKSTLLIPLIFGHVYVMAFFP- 363  
Qy 274 TEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSRWTL--ALDFKKA 331  
Db 364 ---DNFAQKQVNFVVGSGFQGFVAILIYFCNGEVOAEIRKWRWRHQLGVLGWSKS 420  
Qy 332 R---SGSSYSYGMVMSHTSVTVNGPRA 356  
Db 421 QHPWGGSGNGATCSTQVS--MLTRVSPSA 446

RESULT 8  
S16319  
secretin receptor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S16319  
R;Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.  
EMBO J. 10, 1635-1641, 1991  
A;Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.  
A;Reference number: S16319; MUID:91266890; PMID:1646711  
A;Accession: S16319  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-449 <ISH>  
A;Cross-references: UNIPROT:P23811; EMBL:X59132; NID:g57228; PIDN:CAA41849.1; PID:g57229  
C;Superfamily: glucagon receptor  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 33.2%; Score 757.5; DB 2; Length 449;  
Best Local Similarity 44.8%; Pred. No. 2.7e-55;  
Matches 154; Conservative 64; Mismatches 87; Indels 39; Gaps 9;

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QY 22 AVALEVDFRLGMIYTVGYGSMASLTVAVLILAYFRRLHCTRNYYIHMFSLFPMRAASI 81
Db 137 AYLL-----KLKMYITVGYSSMLLVALSLILCSFRLRLHCTRNYYIHMLFVSLFRLALSN 192
QY 82 FVKDAVLVSGFTLDEARLTETELHIIAQVPPPPAAAVGAGCRVAVTFVFLYFLATNY 141
Db 193 FIKDAVLS-----SDDVTYCDAHKV-----GCKLVMIFFQYCIWANYA 231
QY 142 WLLVEGLYLHSLIFMAFSEKYLKMGFTIFGWLPAFVAVVWGVVATLANTGCDWLSGG 201
Db 232 WLLVEGLYLHSLIFMAFSEKYLKMGFTIFGWLPAFVAVVWGVVATLANTGCDWLSGG 201
QY 202 HKK-WIIQVILASVNLFIINIRVLATKLRNAGRCDCRQYKRLRLSTLVLVPL 260
Db 292 ASVWVIRGVPVLSILNIFINIRILMRKLR-TQETRGSETHYKRLAKSTLLTLLPL 350
QY 261 FGVHYTVFMAFVTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKWSNR 320
Db 351 FGIHYIVFAFSPEDAM-----EVQLFFELALGSFQGLVAVLYCFLNGEVQLEVKWKRRQ 405
QY 321 WTLALDFRKARSGSSYS-----YGMVSHTSVTNVG-----PRAGL 358
Db 406 WHLQ-EFFLRPVAFNNSFNATGPTHSTKASTEQSRISIPRASI 448
RESULT 9
JC2532
secretin receptor - human
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C:Accession: JC2532
R:Jiang, S.; Ulrich, C.
Biochem. Biophys. Res. Commun. 207, 883-890, 1995
A:Title: Molecular cloning and functional expression of a human pancreatic secretin rece
A:Reference number: JC2532; MUID:95169147; PMID:7864894
A:Accession: JC2532
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-440 <JTA>
A:Cross-references: UNIPROT:P47872; EMBL:U20178; NID:G662795; PIDN:AAC50106.1; PID:G6627
A:Experimental source: pancreas
C:Genetics:
A:Gene: GDB:SCFR
A:Cross-references: GDB:270546; OMIM:182098
A:Map position: 2q14.1-2q14.1
C:Superfamily: glucagon receptor
Query Match 32.6%; Score 745; DB 2; Length 440;
Best Local Similarity 48.8%; Pred. No. 2.9e-54;
Matches 145; Conservative 50; Mismatches 70; Indels 32; Gaps 5;
QY 30 RLGMIVTVGYGSMASLTVAVLILAYFRRLHCTRNYYIHMFSLFPMRAASIFVKDAVLY 89
Db 141 KLKMYITVGYSSMLLVALSLILCSFRLRLHCTRNYYIHMLFVSLFRLALSNFIKDAVLF 200
QY 90 SG--FTLDEARLTETELHIIAQVPPPPAAAVGAGCRVAVTFVFLYFLATNYWILVEG 147
Db 201 SSDVTVCDAR-----AGCKLVMLFQYCIWANYSWLLVVEG 237
QY 148 LYLHSLIFMAFSEKYLKMGFTIFGWLPAFVAVVWGVVATLANTGCDWLSGGHK-KWI 206
Db 238 LYLHSLIFMAFSEKYLKMGFTIFGWLPAFVAVVWGVVATLANTGCDWLSGGHK-KWI 206
QY 207 IQVILASVNLFIINIRVLATKLRNAGRCDCRQYKRLRLSTLVLVPLFGVHYT 266
Db 298 IRGVPVLSILNIFINIRILMRKLR-TQETRGSETHYKRLAKSTLLTLLPLFGIHYI 356
QY 267 VEMALPTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKWSNRWTL 323
Db 357 VFAPSPEDAM-----EQLFFELALGSFQGLVAVLYCFLNGEVQLEVKWKQQHML 408
RESULT 10
```

JC2194

vasoactive intestinal peptide receptor precursor - human

C:Species: Homo sapiens (man)

C&gt;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

C:Accession: JC2194; JN0604; PC2289; S38397

R:Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Denis

Biochem. Biophys. Res. Commun. 200, 769-776, 1994

A:Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA en

A:Reference number: JC2194; MUID:94235025; PMID:8179610

A:Accession: JC2194

A:Molecule type: mRNA

A:Residues: 1-460 &lt;COH&gt;

A:Cross-references: UNIPROT:P32241; EMBL:X75299; NID:G407461; PIDN:CAAS3046.1; PID:G4074

A:Experimental source: jejunal epithelial cell; clone hIVR8

R:Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.

Biochem. Biophys. Res. Commun. 193, 546-553, 1993

A:Title: Cloning and functional expression of a human neuroendocrine vasoactive intestin

A:Reference number: JN0604; MUID:93290641; PMID:8390245

A:Accession: JN0604

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-284,288-460 &lt;GRE&gt;

A:Cross-references: GB:L13288; NID:G292903; PIDN:AAA36805.1; PID:G292904

R:Couvineau, A.; Gaudin, P.; Maoret, J.J.; Rouyer-Fessard, C.; Nicole, P.; Laburthe, M.

Biochem. Biophys. Res. Commun. 206, 246-252, 1995

A:Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-terminal

A:Reference number: PC2289; MUID:95118345; PMID:7818527

A:Accession: PC2289

A:Molecule type: mRNA

A:Residues: 63-129 &lt;CO2&gt;

C:Genetics:

A:Gene: GDB:VIPR1; RCD1; HVR1

A:Cross-references: GDB:128589; OMIM:192321

A:Map position: 3p22-3p22

C:Superfamily: glucagon receptor

C:Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane prot

F:1-30/Domain: signal sequence #status predicted &lt;SIG&gt;

F:31-460/Product: vasoactive intestinal peptide receptor #status predicted &lt;MAT&gt;

F:145-168/Domain: transmembrane #status predicted &lt;TM1&gt;

F:176-194/Domain: transmembrane #status predicted &lt;TM2&gt;

F:216-234/Domain: transmembrane #status predicted &lt;TM3&gt;

F:255-277/Domain: transmembrane #status predicted &lt;TM4&gt;

F:299-319/Domain: transmembrane #status predicted &lt;TM5&gt;

F:346-363/Domain: transmembrane #status predicted &lt;TM6&gt;

F:377-396/Domain: transmembrane #status predicted &lt;TM7&gt;

F:58,69,100,293/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted

F:250/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

F:450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 32.5%; Score 741; DB 2; Length 460;

Best Local Similarity 45.2%; Pred. No. 6.5e-54;

Matches 149; Conservative 58; Mismatches 87; Indels 36; Gaps 8;

QY 35 YTVGYGSMASLTVAVLILAYFRRLHCTRNYYIHMFSLFPMRAASIFVKDAVLYSGFTL 94

Db 146 YTVGYGSMASLTVAVLILAYFRRLHCTRNYYIHMFSLFPMRAASIFVKDAVLYSGFTL 94

QY 95 DEARLTETELHIIAQVPPPPAAAVGAGCRVAVTFVFLYFLATNYWILVEGLYLHSLI 154

Db 203 GESDQCS-----GSVCKAMVFFQYCVANFFMLVVEGLYLHSLI 244

QY 155 FMAFFSEKYLKMGFTIFGWLPAFVAVVWGVVATLANTG---CWDLSGGHKWIIQVPI 211

Db 245 AVSFFSEKYLKMGFTIFGWLPAFVAVVWGVVATLANTG---CWDLSGGHKWIIQVPI 211

QY 212 LASVNLFIINIRVLATKLRNAGRCDCRQYKRLRLSTLVLVPLFGVHYTVFMA 271

Db 305 LTSILNFIINIRVLATKLRNAGRCDCRQYKRLRLSTLVLVPLFGVHYTVFMA 271

QY 272 PYTEVSGTLWQIOMHYEMLFNSFGQFVVAIYFCNGEVOAEIRKWSNRWTL--ALDFK 329

Db 364 P-----DNFKEVKNVFEVVGSGFQGLVAVLYCFLNGEVOAEIRKWSNRWTL--ALDFK 329

330 KAR---SGSSSYSGPWSHSTVTVNGPRA 356  
 420 KYRHPGSGNGATCTQVS--MLTRVSPGA 447

RESULT 11  
 JC2195  
 vasoactive intestinal peptide receptor-related protein precursor (clone hIVRS) - human  
 C;Species: Homo sapiens (man)  
 C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 24-Nov-1999  
 C;Accession: J02195; S42087  
 R;Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carreto, I.; Ogier-Denis  
 Biochem. Biophys. Res. Commun. 200, 769-776, 1994  
 A;Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA en  
 A;Reference number: JC2194; MUID:94235025; PMID:8179610  
 A;Accession: JC2195  
 A;Molecule type: mRNA  
 A;Residues: 1-495 <COU>  
 A;Cross-references: EMBL:X77777; NID:g456352; PIDN:CAA54814.1; PID:g456353  
 A;Experimental source: jejunal epithelial cell  
 C;Genetics:  
 A;Gene: GDB:VIPR1; RCD1; HVR1  
 A;Cross-references: GDB:128589; OMIM:192321  
 A;Map position: 3p22-3p22  
 C;Superfamily: glucagon receptor  
 C;Keywords: glycoprotein; intestine; phosphoprotein; receptor; transmembrane protein  
 F;1-31/Domain: signal sequence #status predicted <SIG>  
 F;32-495/Product: vasoactive intestinal peptide receptor-related protein #status predict  
 F;180-203/Domain: transmembrane #status predicted <TM1>  
 F;211-229/Domain: transmembrane #status predicted <TM2>  
 F;251-269/Domain: transmembrane #status predicted <TM3>  
 F;290-312/Domain: transmembrane #status predicted <TM4>  
 F;334-354/Domain: transmembrane #status predicted <TM5>  
 F;412-431/Domain: transmembrane #status predicted <TM6>  
 F;381-398/Domain: transmembrane #status predicted <TM7>  
 F;93,104,135,328/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F;111/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted  
 F;285/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted  
 F;485/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 32.5%; Score 741; DB 2; Length 495;  
 Best Local Similarity 45.2%; Pred. No. 7.1e-54;  
 Matches 149; Conservative 58; Mismatches 87; Indels 36; Gaps 8;

35 YTVGYMSLASLTAVLILAYFRRLHCTRNYYIHMFSLFMLRAASIFVKDVLVSGFTL 94  
 181 YTVGYMSLASLTAVLILAYFRRLHCTRNYYIHMFSLFMLRAASIFVKDVLVSGFTL 94

95 DEARLTTELHIIAQVPPPPAAAAGVAGCRVAVTFEFLYFLATNYYWILVEGLYLHSLI 154  
 238 GESDQCSE-----GSVCKAAWVFQVCWMAWFWLVEGLYLHSLI 279

155 FMAFFSEKYLWGFTIFGWLPAVFVAVWVGVRATLANTG---CWDLSGSKHKKWIIQVPI 211  
 280 AVSFFSEKYLWGFTIFGWLPAVFVAVWVGVRATLANTG---CWDLSGSKHKKWIIQVPI 211

212 LASVNLFIPIIRIVLTKLRETNAQCDTROQYRKLRSTLVLPFGVHYTVFMALP 271  
 340 LTSILNFIPIIRIVLTKLRETNAQCDTROQYRKLRSTLVLPFGVHYTVFMALP 271

272 PYTEVSGTLWQIOMHYEMLFNSFOGFFVAILIYCFNCEVQAEIRKMSRWTL--ALDFKR 329  
 399 P-----DNFKPEVKMVFELVVGSGFGFVAILIYCFNCEVQAEIRKMSRWTL--ALDFKR 329

330 KAR---SGSSSYSGPWSHSTVTVNGPRA 356  
 455 KYRHPGSGNGATCTQVS--MLTRVSPGA 482

RESULT 12  
 JN0902  
 pituitary adenylate cyclase activating peptide receptor type I precursor - human

C;Species: Homo sapiens (man)  
 C;Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 20-Jun-2000  
 C;Accession: JN0902  
 R;Ogi, K.; Miyamoto, Y.; Masuda, Y.; Habata, Y.; Hosoya, Y.; Ohtaki, T.; Masuo, Y.; Onda  
 Biochem. Biophys. Res. Commun. 196, 1511-1521, 1993  
 A;Title: Molecular cloning and functional expression of a cDNA encoding a human pituitary  
 A;Reference number: JN0902; MUID:94071918; PMID:7902709  
 A;Accession: JN0902  
 A;Molecule type: mRNA  
 A;Residues: 1-525 <OGI>  
 A;Cross-references: DDBJ:DL7516; NID:g457562; PIDN:BAA04466.1; PID:g540518  
 A;Experimental source: pituitary  
 C;Comment: This protein plays pivotal roles as a neurotransmitter and a neuromodulator,  
 C;Superfamily: glucagon receptor  
 C;Keywords: glycoprotein; neurotransmitter; receptor  
 F;1-77/Domain: signal sequence #status predicted <SIG>  
 F;78-525/Product: pituitary adenylate cyclase activating peptide receptor type I #status  
 F;105,117,174,357,400,432/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 30.1%; Score 687; DB 2; Length 525;  
 Best Local Similarity 40.1%; Pred. No. 2.4e-49;  
 Matches 134; Conservative 65; Mismatches 89; Indels 46; Gaps 7;

34 IYTVGYMSLASLTAVLILAYFRRLHCTRNYYIHMFSLFMLRAASIFVKDVLVSGFT 93  
 213 IYTVGYMSLASLTAVLILAYFRRLHCTRNYYIHMFSLFMLRAASIFVKDVLVSGFT 93

94 LDEARLTTELHIIAQVPPPPAAAAGVAGCRVAVTFEFLYFLATNYYWILVEGLYLHSL 153  
 270 -----EODSNHCF-----ISTVECKAAWVFQVCWMAWFWLVEGLYLHSL 311

154 IFMAFFSEKYLWGFTIFGWLPAVFVAVWVGVRATLANTGCDLS--SGHKKWIIQVPI 212  
 312 LVETFFPERYFYWIIIGWGTTCVTVWATLRLYFDDTGCDMDNDSTALWVVGKPVV 371

213 ASVNLFIPIIRIVLTKLRETNAQCDTROQYRKLRSTLVLPFGVHYTVFMALP 272  
 372 GSIWNVFLFIPIIRIVLTKLRETNAQCDTROQYRKLRSTLVLPFGVHYTVFMALP 272

273 YTEVSGTLWQIOMHYEMLFNSFOGFFVAILIYCFNCEVQAEIRKMSRWTL---ALDFK 328  
 431 ----ENVSKRELVLVEGLSGFGFVAVVLYCFNCEVQAEIRKMSRWKRYFAVDFFK 486

329 RKARSGSSSYSGPWSHSTVTVNGPRAGLSLPL 362  
 487 HR-----HPSLASSGVNGGQLSLI 505

RESULT 13  
 JN0616  
 pituitary adenylate cyclase-activating polypeptide receptor 46-5 precursor - rat  
 N;Alternate names: PACAP receptor  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
 C;Accession: JN0616; S36768  
 R;Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohtaki, T.; Okazaki, H.; Ari  
 Biochem. Biophys. Res. Commun. 194, 133-143, 1993  
 A;Title: Molecular cloning and functional expression of rat cDNAs encoding the receptor  
 A;Reference number: JN0616; MUID:93326107; PMID:7687425  
 A;Accession: JN0616  
 A;Molecule type: mRNA  
 A;Residues: 1-467 <HOS>  
 A;Cross-references: UNIPROT:P32215  
 A;Experimental source: brain  
 R;Spengler, D.; Waerber, C.; Pantaloni, C.; Holsboer, F.; Bockaert, J.; Seeburg, P.H.; J  
 Nature 365, 170-175, 1993  
 A;Title: Differential signal transduction by five splice variants of the PACAP receptor  
 A;Reference number: S36768; MUID:93326107; PMID:8396727  
 A;Accession: S36768  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-467 <SPE>  
 A;Cross-references: EMBL:Z32279; NID:g404252; PIDN:CAA80817.1; PID:g404253



C:Superfamily: glucagon receptor

C:Keywords: alternative splicing; glycoprotein; receptor

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-467/Product: pituitary adenylate cyclase-activating polypeptide receptor 46-5 #stat

F:47:59,116,299,342,374/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.0%; Score 684; DB 2; Length 467;

Best Local Similarity 40.1%; Pred. No. 3.7e-49;

Matches 134; Conservative 64; Mismatches 90; Indels 46; Gaps 7;

34 IYTVGYMSLASLTAVLILAYFRRLHCTRNVIHMHFSLFMLRAASIFVKDAVLYSGFT 93

155 LYTVGYSTSLATLTAMVILCFRKLHCTRNFIHNNLFVSPMLRAISVFIKDWILYA--- 211

94 LDEAERLTEELHIIAQVPPPPAAAVGACRVAVTFYFLATNYWILVEGLYHLSL 153

212 -----EODSSHCF-----VSTVECKAVMVFHYCVSNFYFLFIEGLYHLSL 253

154 IFMAFFSEKKYLWGFTIFGWLPAVFAVAVGVVRATLANTGCDLS-SGHKKWIIQVPL 212

254 LVETFFPERYFYWTIIWGFTPTVCVTVAVLRLYFDGAGCNDSTALMWVVKGPV 313

213 ASVLNFIILFINIRVLATKLRETNAGRCDTQQYKRLRLSTLVPLFGVHYTVFMALP 272

314 GSIMVNFVFIGIILVQKLPDGMGNES-SIVLRLARSTLLIPLFGIHYTVFASP 372

273 YTEVSGTLWQIQMHYEMFLNSFGQFFVAILIYFCNGEVOAETKWSRWTL-----ALDFK 328

373 ----ENVSQKRELVEFLGELSGQFVAVLYCFLNGEVOAETKRWKSNVNRVETMDFK 428

329 RKARGSSSYSGYPMVSVTVNCGPRAGLSPL 362

429 HR-----HPSLASSGVNGTQLSI 447

RESULT 14

JU0185

PACAP/VIP receptor (PACAPR-3) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004

R:Inagaki, N.; Yoshida, H.; Mizuta, M.; Mizuno, N.; Fujii, Y.; Gonoi, T.; Miyazaki, J.;

Proc. Natl. Acad. Sci. U.S.A. 91, 2679-2683, 1994

A:Title: Cloning and functional characterization of a third pituitary adenylate cyclase-

A:Reference number: A53471; MUID:94195806; PMID:9146174

A:Accession: A53471

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-437 <RES>

A:Cross-references: UNIPROT:P41588; GB:D28132; NID:9473721; PIDN:BA005674.1; PID:9496376

A:Experimental source: strain C57BL/6

C:Superfamily: glucagon receptor

C:Keywords: receptor

Query Match 29.6%; Score 676.5; DB 2; Length 437;

Best Local Similarity 42.0%; Pred. No. 1.4e-48;

Matches 141; Conservative 64; Mismatches 84; Indels 47; Gaps 12;

34 IYTVGYMSLASLTAVLILAYFRRLHCTRNVIHMHFSLFMLRAASIFVKDAVLYSGFT 93

128 IYTLGYSVLSLMTGSIICLFRKLHCTRNVIHNLFLSFLMLRAISVLKDSVLYSSG 187

94 LDEAERLTEELHIIAQVPPPPAAAVGACRVAVTFYFLATNYWILVEGLYHLSL 153

188 L-----LRCHDQPAS-----WVGCKLSLVFFQYCIANFVWLLVEGLYHLSL 229

154 IFMAFFSEKKYLWGFTIFGWLPAVFAVAVGVVRATLANTGCDLS-SGHK--KWIIQVPI 211

230 L-VAILPPSRCLAYLLIGWGISVCGIATRLSLEDTCGWD-TNDHSIPWVIRMPI 287

212 LASVVLNFIILFINIRVLATKLRETNAGRCDTQQYKRLRLSTLVPLFGVHYTVFMAL 271

288 LISIWNVNFALFISIVRIILQKLTSPDVGGND-QSQYKRLAKSTLLIPLFGVHYTVFAAP 346

QY 272 PYTEVSGTLWQIQMHYEMFLNSFGQFFVAILIYFCNGEVOAETKWSW-----SR-- 320

Db 347 P-IGISST---YQILFELCVGSFQGLVAVLYCFLNSEVQCEKLRWRGCLTQAGSRDY 402

QY 321 ----WTIALDFFRKA---RSGSSSYSGYPMVSVTVN 349

Db 403 RLHSHWSMRNGSESALQIHRGSRTOQSF--LQSETSV 436

RESULT 15

S39069

vasoactive intestinal peptide receptor VIP2 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C:Accession: S39069

R:Jutuz, E.M.; Sheward, W.J.; West, K.M.; Morrow, J.A.; Fink, G.; Harmar, A.J.

FEBS Lett. 334, 3-8, 1993

A:Title: The VIP(2) receptor: molecular characterisation of a cDNA encoding a novel rece

A:Reference number: S39069; MUID:94039806; PMID:8224221

A:Accession: S39069

A:Molecule type: mRNA

A:Residues: 1-437 <LUT>

A:Cross-references: UNIPROT:P35000; EMBL:Z25885; NID:9414188; PIDN:CAA81104.1; PID:94141

C:Superfamily: glucagon receptor

C:Keywords: G protein-coupled receptor; intestine; transmembrane protein

Query Match 29.5%; Score 672.5; DB 2; Length 437;

Best Local Similarity 41.8%; Pred. No. 3.1e-48;

Matches 141; Conservative 65; Mismatches 82; Indels 49; Gaps 13;

QY 34 IYTVGYMSLASLTAVLILAYFRRLHCTRNVIHMHFSLFMLRAASIFVKDAVLYSGF- 92

Db 128 IYTLGYSVLSLMTGSIICLFRKLHCTRNVIHNLFLSFLMLRAISVLKDSVLYSSG 187

QY 93 TLDEAERLTEELHIIAQVPPPPAAAVGACRVAVTFYFLATNYWILVEGLYHLS 152

Db 188 TL-----RCHDQPGS-----WVGCKLSLVFFQYCIANFVWLLVEGLYHLS 228

QY 153 LIFMAFFSEKKYLWGFTIFGWLPAVFAVAVGVVRATLANTGCDLS-SGHK--KWIIQVP 210

Db 229 LL-VAILPPSRCLAYLLIGWGISVCGIATRLSLEDTCGWD-TNDHSIPWVIRMP 286

QY 211 ILASVVLNFIILFINIRVLATKLRETNAGRCDTQQYKRLRLSTLVPLFGVHYTVFMA 270

Db 287 ILISIVNWFALFISIVRIILQKLTSPDVGGND-QSQYKRLAKSTLLIPLFGVHYTVFAA 345

QY 271 LPTYEVSGTLWQIQMHYEMFLNSFGQFFVAILIYFCNGEVOAETKWSW-----SR- 320

Db 346 FP-IGISST---YQILFELCVGSFQGLVAVLYCFLNSEVQCEKLRWRGCLTQAGSRD 401

QY 321 ----WTIALDFFRKA---RSGSSSYSGYPMVSVTVN 349

Db 402 YRLHSHWSMRNGSESALQIHRGSRTOQSF--LQSETSV 436

Search completed: November 23, 2004, 20:59:32

Job time : 22 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 23, 2004, 20:59:18 ; Search time 145 Seconds  
(without alignments)  
1062.383 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCCPVLS.....EASGSARPPPLQEGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pdb.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pdb.\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pdb.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pdb.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pdb.\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2195	96.1	591	14	US-10-267-730-20
2	2187	95.8	591	9	US-09-943-446-7
3	2146	94.0	591	9	US-09-943-446-8
4	2008	88.0	593	9	US-09-943-446-9
5	2008	88.0	593	14	US-10-225-567A-229
6	2002	87.7	593	10	US-09-826-509-563
7	2002	87.7	593	14	US-10-267-730-21
8	1957	85.7	595	9	US-09-943-446-6
9	1710	74.9	585	14	US-10-267-730-19
10	1698	74.4	964	14	US-10-017-161-710
11	1698	74.4	964	14	US-10-292-798-622
12	1551	67.9	515	14	US-10-267-730-18
13	1465	64.2	536	14	US-10-372-095-2

14	1130	49.5	542	14	US-10-372-095-4	Sequence 4, Appli
15	1068	46.8	575	14	US-10-372-095-5	Sequence 5, Appli
16	1050.5	46.0	550	14	US-10-225-567A-227	Sequence 227, App
17	1050.5	46.0	550	14	US-10-295-027-526	Sequence 526, App
18	1050.5	46.0	550	14	US-10-295-027-851	Sequence 851, App
19	1050.5	46.0	561	14	US-10-295-027-524	Sequence 524, App
20	1044.5	45.8	550	10	US-09-826-509-565	Sequence 565, App
21	1036	45.4	541	9	US-09-996-569-2	Sequence 2, Appli
22	1028.5	45.1	550	14	US-10-014-162-110	Sequence 110, App
23	1011.5	44.3	546	14	US-10-014-162-109	Sequence 109, App
24	776	34.0	459	16	US-10-831-393-4	Sequence 4, Appli
25	775.5	34.0	1324	9	US-09-935-371-56	Sequence 56, Appli
26	773.5	33.9	444	16	US-10-831-393-6	Sequence 6, Appli
27	772	33.8	459	16	US-10-831-393-3	Sequence 3, Appli
28	772	33.8	459	16	US-10-831-393-8	Sequence 8, Appli
29	762.5	33.4	458	16	US-10-831-393-5	Sequence 5, Appli
30	762.5	33.4	458	16	US-10-831-393-7	Sequence 7, Appli
31	757.5	33.2	449	15	US-10-051-874-68	Sequence 68, Appli
32	752.5	33.0	457	14	US-10-225-567A-469	Sequence 469, App
33	752.5	33.0	457	14	US-10-292-798-618	Sequence 618, App
34	752.5	33.0	457	16	US-10-831-393-1	Sequence 1, Appli
35	747	32.7	440	14	US-10-292-798-608	Sequence 608, App
36	747	32.7	440	15	US-10-051-874-64	Sequence 64, Appli
37	747	32.7	440	15	US-10-051-874-65	Sequence 65, Appli
38	747	32.7	440	15	US-10-398-454-3	Sequence 3, Appli
39	747	32.7	440	15	US-10-398-455-3	Sequence 3, Appli
40	747	32.7	440	15	US-10-398-448-3	Sequence 3, Appli
41	746.5	32.7	457	10	US-09-826-509-579	Sequence 579, App
42	745	32.6	440	15	US-10-051-874-66	Sequence 66, Appli
43	745	32.6	440	15	US-10-051-874-67	Sequence 67, Appli
44	744	32.6	440	14	US-10-225-567A-310	Sequence 310, App
45	741	32.5	460	16	US-10-831-393-2	Sequence 2, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-267-730-20  
; Sequence 20, Application US/10267730  
; Publication No. US20030153041A1  
; GENERAL INFORMATION:  
; APPLICANT: Segre, Gino V.  
; APPLICANT: Kronenberg, Henry M.  
; APPLICANT: Abou-Samra, Abdul-Badi  
; APPLICANT: Juppner, Harald  
; APPLICANT: Potts, Jr., John T.  
; APPLICANT: Schipani, Ernestina  
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME  
; FILE REFERENCE: 00786/071005  
; CURRENT APPLICATION NUMBER: US/10/267,730  
; CURRENT FILING DATE: 2003-01-27  
; PRIOR APPLICATION NUMBER: US 08/471,494  
; PRIOR FILING DATE: 1995-06-06  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 591  
; TYPE: PRT

ORGANISM: Rattus rattus  
US-10-267-730-20

Query Match  
Best Local Similarity 96.1%; Score 2195; DB 14; Length 591;  
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;

Qy	1	MGAARIAPSLALLCCPVLSAYAL	-----25
Db	1	MGAARIAPSLALLCCPVLSAYAL	-----25
Qy	26	-----	25
Db	61	NIMESDKGWTFASTGKPRKEKASGKFPYKSKNDVPTGSRGRPCLPEDNIVCWPL	120

QY 26 ----- 25  
Db 121 GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRWTWANYSECLKFMNTRE 180  
QY 26 -EVFDRGLMITYVGYSMSLASLTAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK 84  
Db 181 REVFDRLGMITYVGYSMSLASLTAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK 240  
QY 85 DAVLYSGFTLDEAERLTERELHIIAQVPPPPAAAAAGYACRVAVTFFLYFLATNYYWIL 144  
Db 241 DAVLYSGFTLDEAERLTERELHIIAQVPPPPAAAAAGYACRVAVTFFLYFLATNYYWIL 300  
QY 145 VEGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVWVVRATLANTGCDLSSGHKK 204  
Db 301 VEGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVWVVRATLANTGCDLSSGHKK 360  
QY 205 WIIOVPTLASVNLFIINIRVLATKLRETNAGRCTDQOYRKLRLSTLVLPLFGVH 264  
Db 361 WIIOVPTLASVNLFIINIRVLATKLRETNAGRCTDQOYRKLRLSTLVLPLFGVH 420  
QY 265 YTFVMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 324  
Db 421 YTFVMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 480  
QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 384  
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 540  
QY 385 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 435  
Db 541 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 591  
RESULT 3  
US-09-943-446-8  
; Sequence 8, Application US/09943446  
; Patent No. US20020146777A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Castleberry, Tessa A.  
; APPLICANT: Lu, Bihong  
; APPLICANT: Owen, Thomas A.  
; APPLICANT: Smock, Steven L.  
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor  
; FILE REFERENCE: PC10891AGR  
; CURRENT APPLICATION NUMBER: US/09/943,446  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 60/229,170  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Mus Musculus  
US-09-943-446-8  
Query Match 94.0%; Score 2146; DB 9; Length 591;  
Best Local Similarity 72.1%; Pred. No. 6e-185;  
Matches 426; Conservative 2; Mismatches 7; Indels 156; Gaps 1;  
QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25  
Db 1 MGTARIAPSLALLCCPVLSSAYALVDADDVFTKEEQIFLLHRAQAQCKLLKEVLHTAA 60  
QY 26 ----- 25  
Db 61 NIMESDKGWTASTSGKPRKEKAPGKFPESKENKDVPTGSRRRGRPCLPWDNIVCWPL 120  
QY 26 ----- 25  
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QY 26 -EVFDRGLMITYVGYSMSLASLTAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK 84  
Db 181 REVFDRLGMITYVGYSMSLASLTAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK 240

QY 26 ----- 25  
Db 121 GAPGEVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRWTWANYSECLKFMNTRE 180  
QY 26 -EVFDRGLMITYVGYSMSLASLTAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK 84  
Db 181 REVFDRLGMITYVGYSMSLASLTAVLILAYFRLHCTRNYIHHMFSLFMLRAASIFVK 240  
QY 85 DAVLYSGFTLDEAERLTERELHIIAQVPPPPAAAAAGYACRVAVTFFLYFLATNYYWIL 144  
Db 241 DAVLYSGFTLDEAERLTERELHIIAQVPPPPAAAAAGYACRVAVTFFLYFLATNYYWIL 300  
QY 145 VEGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVWVVRATLANTGCDLSSGHKK 204  
Db 301 VEGYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVWVVRATLANTGCDLSSGHKK 360  
QY 205 WIIOVPTLASVNLFIINIRVLATKLRETNAGRCTDQOYRKLRLSTLVLPLFGVH 264  
Db 361 WIIOVPTLASVNLFIINIRVLATKLRETNAGRCTDQOYRKLRLSTLVLPLFGVH 420  
QY 265 YTFVMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 324  
Db 421 YTFVMAIPYTEVSGTLWQIQMHYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRWTLA 480  
QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 384  
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 540  
QY 385 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 435  
Db 541 APATETETLPTVMAVPKDDGFLNGSCSGLDEEASGSARPPPLLOEGWETVM 591  
RESULT 2  
US-09-943-446-7  
; Sequence 7, Application US/09943446  
; Patent No. US20020146777A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Castleberry, Tessa A.  
; APPLICANT: Lu, Bihong  
; APPLICANT: Owen, Thomas A.  
; APPLICANT: Smock, Steven L.  
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor  
; FILE REFERENCE: PC10891AGR  
; CURRENT APPLICATION NUMBER: US/09/943,446  
; CURRENT FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 60/229,170  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Rattus No. US20020146777A1vegicus  
US-09-943-446-7  
Query Match 95.8%; Score 2187; DB 9; Length 591;  
Best Local Similarity 73.4%; Pred. No. 1.2e-188;  
Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;  
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Db 1 MGAARIAPSLALLCCPVLSSAYALVDADDVFTKEEQIFLLHRAQAQCKLLKEVLHTAA 60  
QY 26 ----- 25  
Db 61 NIMESDKGWTASTSGKPRKEKASGKFPESKENKDVPTGSRRRGRPCLPWDNIVCWPL 120  
QY 26 ----- 25  
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QY 325 LDFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATTNGHSQPLPGHAKP 383
Db 481 LDFKRKARSGSSSYSGPMVSHTSVTNVGPRVGLPLSPRLPTATTNGHPOLPGHAKP 540
QY 384 GAPTET-ETLPTMAVPKDDGFLNGSCGLDEASGSRPPPLQBGWETVM 435
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RESULT 6
US-09-826-509-563
; Sequence 563, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR FILING DATE: 2000-04-07
; PRIOR FILING DATE: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 563
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-563

Query Match 87.7%; Score 2002; DB 10; Length 593;
Best Local Similarity 67.1%; Pred. No. 6.2e-172; Indels 158; Gaps 3;
Matches 398; Conservative 10; Mismatches 27;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRP 60
QY 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGLYPESEEDKEAPTGSRYGRPCLPEDWHILCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIDFNHKGHAYRCDRNGSWELVPGHNRWTWANYSECVKFLTNETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASITVAVLILAYFRRLHCTRTNYIHMHPFLSFMLRAASIFVK 84
Db 191 REVFDRLGMIYTVGYSVSLASITVAVLILAYFRRLHCTRTNYIHMHPFLSFMLRAVSIFVK 240
QY 85 DAVLYSGTLDABRLTEBELHIHQVPPPPAAAAGVAGCRVATFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDABRLTEELRAIAQAPPPPPATAAGVAGCRVATFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWGVVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWGVVRATLANTGCDLSSGNKK 360
QY 205 WIIQVPIIASVNLNFIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLPLFGVH 264
Db 361 WIIQVPIIASVNLNFIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLPLFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVQAEIRKSWSRWTLA 324
Db 361 WIIQVPIIASVNLNFIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLPLFGVH 420
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QY 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVQAEIRKSWSRWTLA 324
Db 421 YIVFMATPYTEVSGTLWQVOMHYEMLFNSFGQFFVAILIYFCNGEVQAEIRKSWSRWTLA 480
QY 325 LDFKRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPR-LPPATTNGHSQPLPGHAKP 383
Db 481 LDFKRKARSGSSSYSGPMVSHTSVTNVGPRVGLPLSPRLPTATTNGHPOLPGHAKP 540
QY 384 GAPTET-ETLPTMAVPKDDGFLNGSCGLDEASGSRPPPLQBGWETVM 435
Db 541 GTPALETLETPPAMAAPKDDGFLNGSCGLDEASGPERPPALLQBEWETVM 593

RESULT 7
US-10-267-730-21
; Sequence 21, Application US/10267730
; Publication No. US20030153041A1
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, Jr., John T.
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME
; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; CURRENT FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-730-21

Query Match 87.7%; Score 2002; DB 14; Length 593;
Best Local Similarity 67.1%; Pred. No. 6.2e-172; Indels 158; Gaps 3;
Matches 398; Conservative 10; Mismatches 27;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKEVLQRP 60
QY 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGLYPESEEDKEAPTGSRYGRPCLPEDWHILCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIDFNHKGHAYRCDRNGSWELVPGHNRWTWANYSECVKFLTNETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASITVAVLILAYFRRLHCTRTNYIHMHPFLSFMLRAASIFVK 84
Db 191 REVFDRLGMIYTVGYSVSLASITVAVLILAYFRRLHCTRTNYIHMHPFLSFMLRAVSIFVK 240
QY 85 DAVLYSGTLDABRLTEBELHIHQVPPPPAAAAGVAGCRVATFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDABRLTEELRAIAQAPPPPPATAAGVAGCRVATFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWGVVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWGVVRATLANTGCDLSSGNKK 360
QY 205 WIIQVPIIASVNLNFIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLPLFGVH 264
Db 361 WIIQVPIIASVNLNFIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLPLFGVH 420
QY 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVQAEIRKSWSRWTLA 324
Db 361 WIIQVPIIASVNLNFIINIRVLATKLRETNAGRCDTROQYRKLLRSTLVLPLFGVH 420
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Db 421 YIVFMATPYTEVSGTLVQVQHYEMLFNSFGFFVAILIYFCNGEVQAEIKKSNRWTLA 480  
QY 325 LDFKKARSGSSSYSGPMVSHSTVTNVGPRAGLSLPLSPR-LPATTNGHSQLPGHAKP 383  
Db 481 LDFKKARSGSSSYSGPMVSHSTVTNVGPRVGLGLPLSPRLPTATTNGHPQLPGHAKP 540  
QY 384 GAPATET-ETLPLVTMAVPKDDGFLNGSCGLDEEASGSARPPPLLOEGWETVM 435  
Db 541 GTPALETLETPPMAAPKDDGFLNGSCGLDEEASGPRPPALLQEEWETVM 593

## RESULT 8

US-09-943-446-6  
; Sequence 6, Application US/09943446  
; Patent No. US2002014677A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: Castleberry, Tessa A.  
; APPLICANT: Lu, Bihong  
; APPLICANT: Owen, Thomas A.  
; APPLICANT: Smock, Steven L.  
; TITLE OF INVENTION: Canine Parathyroid Hormone 1 Receptor  
; FILE REFERENCE: PC10891AGR  
; CURRENT APPLICATION NUMBER: US/09/943,446  
; PRIOR FILING DATE: 2001-08-30  
; PRIOR APPLICATION NUMBER: US 60/229,170  
; PRIOR FILING DATE: 2000-08-30  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 595  
; TYPE: PRT  
; ORGANISM: Canis Familiaris  
US-09-943-446-6

Query Match 85.7%; Score 1957; DB 9; Length 595;  
Best Local Similarity 65.6%; Pred. No. 7,3e-168;  
Matches 394; Conservative 11; Mismatches 24; Indels 172; Gaps 5;  
QY 1 MGARIAPSLALLCCPVLSSAYAL----- 25  
Db 1 MGAVRIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQACQKRLKEVLQRP 60  
QY 26 ----- 25  
Db 61 DIMESDKWASASTSGKPKKXKASGLYSEEDKEVPTGSHRGRCPLPEWDHILCWPL 120  
QY 26 ----- 25  
Db 121 GAPGBVAVPCDXYIDFNHKGHAYRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180  
QY 26 -EVFDRLGMIYTVGYSMSLASLTVAVLILAYPRRLHCTRTNYIHMHFLSPMLRAASIFVK 84  
Db 181 REVFDRLGMIYTVGYSVSLASLTVAVLILAYPRRLHCTRTNYIHMHFLSFLMLRAVSIFVK 240  
QY 85 DAVLYSGFTDEARELLEEELHIIAQVPPPPAAAAGVAGCVAVTFELYFLATNYWIL 144  
Db 241 DAVLYSGATLDEARELLEEELRAIAQAPPPPTAAA-GYAGCRVAVTFELYFLATNYWIL 299  
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVWVVRATLANTGCWDLSSGHKK 204  
Db 300 VEGLYLHSLIFMAFFSEKKYLWGFTVFGWGLPAVFAVAVVSVRATLANTGCWDLSSGNKK 359  
QY 205 WIIQVPILASVVLNFIINIRVLATKLRETNAGRCDCRQYRKLRLSTLVLVPLFGVH 264  
Db 360 WIIQVPILASVVLNFIINIRVLATKLRETNAGRCDCRQYRKLRLSTLVLVPLFGVH 419  
QY 265 YTFWALPYTEVSGTLWQIQHYEMLFNSFGFFVAILIYFCNGEVQAEIKKSNRWTLA 324  
Db 420 YIVFMATPYTEVSGTLVQVQHYEMLFNSFGFFVAILIYFCNGEVQAEIKKSNRWTLA 479  
QY 325 LDFKKARSGSSSYSGPMVSHSTVTNVGPRAGLSLPLSPRPP-----ATTNGHSQL 377

Db 480 LDFKKARSGSSSYSGPMVSHSTVTNVGPRAGLSLPLSPRLPAAAAATTATTNGHPPI 539  
QY 378 PGHAKPGAPATETETLPVT---MAYPKDDGFLNGSCGLDEEASGSARPPPLLOEGWETV 434  
Db 540 PGHTRPGAP----TLPATPPATAAPKDDGFLNGSCGLDEEASAPERPPALLQEEWETV 594  
QY 435 M 435  
Db 595 M 595

## RESULT 9

US-10-267-730-19  
; Sequence 19, Application US/10267730  
; Publication No. US20030153041A1  
; GENERAL INFORMATION:  
; APPLICANT: Segre, Gino V.  
; APPLICANT: Kronenberg, Henry M.  
; APPLICANT: Abou-Samra, Abdul-Badi  
; APPLICANT: Juppner, Harald  
; APPLICANT: Potts, Jr., John T.  
; APPLICANT: Schipani, Ernestina  
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME  
; FILE REFERENCE: 00786/071005  
; CURRENT APPLICATION NUMBER: US/10/267,730  
; CURRENT FILING DATE: 2003-01-27  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: US 08/471,494  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Didelphoidea  
US-10-267-730-19

Query Match 74.9%; Score 1710; DB 14; Length 585;  
Best Local Similarity 80.2%; Pred. No. 1.5e-145;  
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;  
QY 26 EVFDRLGMIYTVGYSMSLASLTVAVLILAYPRRLHCTRTNYIHMHFLSPMLRAASIFVKD 85  
Db 179 EVFDRLGMIYTVGYSISLGSUTVAVLILGYPRRLHCTRTNYIHMHLFVSFMLRAVSIFIKD 238  
QY 86 AVLXSGFTLDEARELLEEELHIIAQVPPPPAAAAGVAGCRVAVTFELYFLATNYWILV 145  
Db 239 AVLXSGVSTDEIERITEBELRAFT-PPADKA-GFVGCRVAVTVFLYFLTNYWILV 295  
QY 146 EGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFAVAVVWVVRATLANTGCWDLSSGHKK 205  
Db 296 EGLYLHSLIFMAFFSEKKYLWGFTLFGWGLPAVFAVAVVTVRATLANTECWDLSSGNKK 355  
QY 206 IIOVPILASVVLNFIINIRVLATKLRETNAGRCDCRQYRKLRLSTLVLVPLFGVHY 265  
Db 356 IIOVPILAAIVVNFILFIINIRVLATKLRETNAGRCDCRQYRKLRLSTLVLVPLFGVHY 415  
QY 266 YTFWALPYTEVSGTLWQIQHYEMLFNSFGFFVAILIYFCNGEVQAEIRKSNRWTLAL 325  
Db 416 IVFNATPYTEVSGILWQVQHYEMLFNSFGFFVAILIYFCNGEVQAEIKKSNRWTLAL 475  
QY 326 DFKKARSGSSSYSGPMVSHSTVTNVGPRAGLSLPLSPRPP---ATTNGHSQLPGHAK 382  
Db 476 DFKKARSGSSSYSGPMVSHSTVTNVGPRGLALSLSPLAPAGAGASANGHQLPGYVK 535  
QY 383 PGAPATETETLPVTMAVP--KDDGFLNGSCGLDEEASGSARPPPLLOEGWETVM 435  
Db 536 HG--SISENLSPSSGPEPTGDKDGLNG--SGLYPMVGE-QPPPLLEEREETVM 585

## RESULT 10

US-10-017-161-710  
; Sequence 710, Application US/10017161  
; Publication No. US20030143668A1

```

; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 710
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-710

Query Match      74.4%; Score 1698; DB 14; Length 964;
Best Local Similarity 59.9%; Pred. No. 3.5e-144;
Matches 356; Conservative 11; Mismatches 31; Indels 196; Gaps 9;

QY 26 EVFDRLGMIYTVGYSMSLASLITVAVLILAYF-----RRLHCTRNYYIHMMFLSFMLRAASIF 82
Db 317 EVFDRLGMIYTVGYSMSLASLITVAVLILAYFRWAGRGERRRDMVGGWRPERSDATPSLHP 376

QY 57 -----RRLHCTRNYYIHMMFLSFMLRAASIF 82
Db 377 SPAGVPTYGAQPSFLSTHRASPCPHRSCRAPRRLHCTRNYYIHMMFLSFMLRAVSIF 436

QY 83 VKDAVLYSGTGLDEAERLTHEELHI IAQVPPPPAAAAGVAG----- 124
Db 437 VKDAVLYSGATLDEAERLTHEELRAIAQAAPPPATAAGVYSTPLPARSCRHWPRGAPP 496

QY 125 -----CR----- 126
Db 497 RPAPRSPCPPPASATGFSHNSPSYRVPNPQLCRPCCOGLRVSHTPRAAIKAPTSTQ 556

QY 127 VAVTFFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFAVVAWVGV 186
Db 557 VAVTFFLYFLATNYWILVEGLYLHSLIFMAFFSEKKYLMGFTVFGWLPAVFAVVAWVSV 616

QY 187 RATLANTGCWDLSSGHKKWIIQVPLASV--LNFIILFINIRVLATKLRETNAGRCDDR 244
Db 617 RATLANTG-----VQPPDAAPSLPQLNFILFINIRVLATKLRETNAGRCDDR 664

QY 245 QQY-----RKLRLSTLVLPVLFVGHVYTFMALPYTEVSGTLWQIQMHYEML 290
Db 665 QQYRGSGALTYLPRWRPRKLLKSTLVLMPLFGVHYIVFMATPYTEVSGTLWQVQMYEML 724

QY 291 FNSF-----QGFVFAIYYFCNGEVAEIRKSWSRWTL 323
Db 725 FNSFQVRSAGPLAEGGSGGRDPSRHPSSQGFVFAIYYFCNGEVAEIRKSWSRWTL 784

QY 324 ALDFKRVKARGSSSYSGPMVSHTSVTNVPGRAGLSLPLSPR-LPPATTNGHSQLPGHAK 382
Db 785 ALDFKRVKARGSSSYSGPMVSHTSVTNVPGRVGLPLSPRLPLPTATTNGHSQLPGHAK 844

QY 383 PGAPATET-ETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGMETVM 435
Db 845 PGTPALETLETTTPMAAPKDDGFLNGSCGLDEASGSARPPALLQEEWETVI 898

RESULT 11
US-10-292-798-622
; Sequence 622, Application US/10292798
; Publication No. US20030235833A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME

; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA ENCODING SAME

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; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-18

Query Match
Best Local Similarity 67.9%; Score 1551; DB 14; Length 515;
Matches 291; Conservative 18; Mismatches 24; Indels 3; Gaps 2;

QY 26 EVFDRGLMIYTVGYSMISLASLTAVLILAYFRLHCTRNYYIHMHFSLPMLRAASIFVKD 85
DB 179 EVFDRGLMIYTVGYSMISLASLTAVLILAYFRLHCTRNYYIHMHFSLPMLRAASIFVKD 238
QY 86 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAGVACRVAVTFFLYFLATNYYWILV 145
DB 239 AVLYSGVSTDEITERITEELRAFTF--PPADKA-GFVGCRAVTVFLYFLATNYYWILV 295
QY 146 EGLYLHSLIFMAFFSEKKYLWGTFTFGWGLPAFVAVVWVGRATLANTCGDLSGSHKKW 205
DB 296 EGLYLHSLIFMAFFSEKKYLWGTFTFGWGLPAFVAVVWVGRATLANTCGDLSGSHKKW 355
QY 206 IIQVPIIASVNLNFIINIRVATKLRETNAGRCDTROQYRKLLRSLTVLPLFGVHY 415
DB 356 IIQVPIIASVNLNFIINIRVATKLRETNAGRCDTROQYRKLLRSLTVLPLFGVHY 415
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKSWSRWTLL 325
DB 416 IVFMATPYTEVSGTLWQIQMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKSWSRWTLL 475
QY 326 DFKRKARSGSSSYGPMVSHTSVTNVGPRAGLSLP 361
DB 476 DFKRKARSGSSSYGPMVSHTSVTNVGPRGWP 511

RESULT 13
US-10-372-095-2
; Sequence 2, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-2

Query Match
Best Local Similarity 64.2%; Score 1465; DB 14; Length 536;
Matches 284; Conservative 45; Mismatches 66; Indels 18; Gaps 4;

QY 26 EVFDRGLMIYTVGYSMISLASLTAVLILAYFRLHCTRNYYIHMHFSLPMLRAASIFVKD 85
DB 139 EVFDRGLMIYTVGYSMISLASLTAVLILAYFRLHCTRNYYIHMHFSLPMLRAASIFVKD 198

; FILE REFERENCE: 00786/071005
; CURRENT APPLICATION NUMBER: US/10/267,730
; PRIOR FILING DATE: 2003-01-27
; PRIOR APPLICATION NUMBER: US 08/471,494
; PRIOR FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Didelphoidea
US-10-267-730-18

Query Match
Best Local Similarity 67.9%; Score 1551; DB 14; Length 515;
Matches 291; Conservative 18; Mismatches 24; Indels 3; Gaps 2;

QY 26 EVFDRGLMIYTVGYSMISLASLTAVLILAYFRLHCTRNYYIHMHFSLPMLRAASIFVKD 85
DB 179 EVFDRGLMIYTVGYSMISLASLTAVLILAYFRLHCTRNYYIHMHFSLPMLRAASIFVKD 238
QY 86 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAGVACRVAVTFFLYFLATNYYWILV 145
DB 239 AVLYSGVSTDEITERITEELRAFTF--PPADKA-GFVGCRAVTVFLYFLATNYYWILV 295
QY 146 EGLYLHSLIFMAFFSEKKYLWGTFTFGWGLPAFVAVVWVGRATLANTCGDLSGSHKKW 205
DB 296 EGLYLHSLIFMAFFSEKKYLWGTFTFGWGLPAFVAVVWVGRATLANTCGDLSGSHKKW 355
QY 206 IIQVPIIASVNLNFIINIRVATKLRETNAGRCDTROQYRKLLRSLTVLPLFGVHY 415
DB 356 IIQVPIIASVNLNFIINIRVATKLRETNAGRCDTROQYRKLLRSLTVLPLFGVHY 415
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKSWSRWTLL 325
DB 416 IVFMATPYTEVSGTLWQIQMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKSWSRWTLL 475
QY 326 DFKRKARSGSSSYGPMVSHTSVTNVGPRAGLSLP 361
DB 476 DFKRKARSGSSSYGPMVSHTSVTNVGPRGWP 511

RESULT 14
US-10-372-095-4
; Sequence 4, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Danio rerio
US-10-372-095-4

Query Match
Best Local Similarity 49.5%; Score 1130; DB 14; Length 542;
Matches 230; Conservative 49; Mismatches 74; Indels 34; Gaps 7;

QY 26 EVFDRGLMIYTVGYSMISLASLTAVLILAYFRLHCTRNYYIHMHFSLPMLRAASIFVKD 85
DB 136 EVFDRGLMIYTVGYSMISLASLTAVLILAYFRLHCTRNYYIHMHFSLPMLRAASIFVKD 195
QY 86 AVLYSGFTLDEAERLITEELHIIAQVPPPPAAAGVACRVAVTFFLYFLATNYYWILV 145
DB 196 AVLYAVNDGELEDAVEQRPV-----GCKAAVTLFYLATNYYWILV 240
QY 146 EGLYLHSLIFMAFFSEKKYLWGTFTFGWGLPAFVAVVWVGRATLANTCGDLSGSHKKW 205
DB 241 EGLYLHSLIFMAFFSEKKYLWGTFTFGWGLPAFVAVVWVGRATLANTCGDLSGSHKKW 300
QY 206 IIQVPIIASVNLNFIINIRVATKLRETNAGRCDTROQYRKLLRSLTVLPLFGVHY 265
DB 301 IIQVPIIASVNLNFIINIRVATKLRETNAGRCDTROQYRKLLRSLTVLPLFGVHY 360
QY 266 TVFMALPYTEVSGTLWQIQMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKSWSRWTLL 325
DB 361 MLFWALPYTDTGLRLQLMHYEMLFNSQGFVVAIIYFCNGEVOAEIRKSWSRWTLL 420
QY 326 DFKRKARSGSSSYGPMVSHTSVTNV-----GPRAGLSLP 376
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Db 421 DLKQKARVHSSACGSGYGGMMSHHTTQSVCLSVSGAKGHSU-----HTIGAKGQSHLQ 476  
QY 377 LPHGAKFGAPATETIL--EVTMAVPK 401  
Db 477 HSGNL-PGYAPQDTEILFYFV--VPK 499

RESULT 15  
US-10-372-095-5  
; Sequence 5, Application US/10372095  
; Publication No. US20030162256A1  
; GENERAL INFORMATION:  
; APPLICANT: Juppner, Harald  
; APPLICANT: Rubin, David A.  
; TITLE OF INVENTION: PTHR and PTHR Receptors, Methods and Uses Thereof  
; FILE REFERENCE: 0609.4740002  
; CURRENT APPLICATION NUMBER: US/10/372,095  
; CURRENT FILING DATE: 2003-02-25  
; PRIOR APPLICATION NUMBER: 09/449,632  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: US 60/110,467  
; PRIOR FILING DATE: 1998-11-30  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Danio rerio  
US-10-372-095-5

Query Match 46.8%; Score 1068; DB 14; Length 575;  
Best Local Similarity 50.9%; Pred. No. 1.5e-87;  
Matches 215; Conservative 71; Mismatches 106; Indels 30; Gaps 8;  
QY 28 FDRIGMIYTVGYSMLASLTAVLILAYFRLHCHTRNYIHMHMFLSPMLRAASIFVKDAV 87  
Db 169 FERLHMYTVGYAVSFSLVAIFIGYFRLHCHTRNYIHMHMFLSPMLRAASIFVKDHY 228  
QY 88 LYSGFTLDEARLFEELHIIAQVPPPPAAAAGVAGCRVATFFLYPLATNYIWLVEG 147  
Db 229 VHTSAGLQESDAVLMMNFTNAVDVAPVDTSQ---YMGCKVTLLFIYPLATNYIWLVEG 285  
QY 148 LYLHSLIFMAFFSEKKYLWGTFIYGWGLPAYVAVVWVVRATLANTCGWDLSSGKKWII 207  
Db 286 LYLHSLIFMAFLSDSKYLWGFTLIGWGPVAVFAAWAVVRATLADARCWELSGAGNIXIY 345  
QY 208 QVPILASVLNFIILFIRVATKLRETNAGRCDTROQYRKLRLSTLVLVPLFGVHYTV 267  
Db 346 QEPILTAIGLNFILFVNIIVRLATKIRETNGRVDTRQYRKLAKSTQVLVFGVHYIV 405  
QY 268 FMALPYTEVSGTLQIOHMYEMLFNSFGFFVAILIYFCNGEVOAEIRKSWRMTLALDF 327  
Db 406 FVGMFHT--FEGLGWEERMYCELFFNSFQGFVSVIICYCNGEVQTEIKKTWRNLAPDW 464  
QY 328 KKKARSSSSSYSGPMV-----SHTSVTVNGPRAGLSLPLSPLEPPA-----TTNGHS 375  
Db 465 KGPVVCGSN--RYGSLVTGLNNSTSSQSLAAGGPGTGTTLFSSRVYRSGGPTVSTHA 522  
QY 376 QLPGHAKFGAPATETITLPTVMAVPKDDGFLNGSCGLDE---EASGSGARPPPLIQEGWE 432  
Db 523 TLPGVVL-----NSDADSLPPSIPPEPED-----SAKQVDDILLKESLPTRPSSGLEDDDEE 573  
QY 433 TV 434  
Db 574 TL 575

Search completed: November 23, 2004, 21:11:11  
Job time : 148 secs

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OM protein - protein search, using sw model

Run on: November 23, 2004, 20:51:44 ; Search time 39 Seconds  
(without alignments)  
739.701 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGAARIAPSLALLCPVL.....EASGARPPPLQBGWETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
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- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2195	96.1	591	2	US-08-468-249A-20
2	2008	88.0	593	4	US-09-631-603-21
3	2002	87.7	593	2	US-08-468-249A-21
4	1710	74.9	585	1	US-08-142-439A-6
5	1710	74.9	585	2	US-08-142-551B-125
6	1710	74.9	585	2	US-08-869-477-6
7	1710	74.9	585	2	US-08-468-249A-19
8	1551	67.9	515	2	US-08-468-249A-18
9	1465	64.2	536	4	US-09-449-632-2
10	1130	49.5	542	4	US-09-449-632-4
11	1068	46.8	575	4	US-09-449-632-5
12	1050.5	46.0	550	4	US-09-631-603-20
13	1036	45.4	541	3	US-08-468-011A-2
14	1036	45.4	541	3	US-09-236-468A-2
15	1036	45.4	541	5	PCT-US95-07085-2
16	960.5	42.1	207	4	US-08-811-519-31
17	776	34.0	459	4	US-09-694-519-4
18	775.5	34.0	1324	2	US-08-811-897A-56
19	775.5	34.0	1324	3	US-09-201-474-56
20	773.5	33.9	444	4	US-09-694-519-6
21	772	33.8	459	4	US-09-694-519-3
22	772	33.8	459	4	US-09-694-519-8
23	762.5	33.4	458	1	US-08-112-817C-2
24	762.5	33.4	458	4	US-09-694-519-5
25	762.5	33.4	458	4	US-09-694-519-7
26	757.5	33.2	449	1	US-08-142-439A-5
27	757.5	33.2	449	2	US-08-869-477-5

28 752.5 33.0 457 4 US-09-631-603-23 Sequence 23, Appl  
29 752.5 33.0 457 4 US-09-694-519-1 Sequence 1, Appl  
30 747 32.7 440 4 US-09-631-603-22 Sequence 22, Appl  
31 741 32.5 460 4 US-09-694-519-2 Sequence 2, Appl  
32 718 31.4 447 4 US-09-694-519-9 Sequence 9, Appl  
33 687 30.1 448 2 US-08-811-897A-22 Sequence 22, Appl  
34 687 30.1 448 2 US-08-855-213-22 Sequence 22, Appl  
35 687 30.1 448 3 US-09-201-474-22 Sequence 19, Appl  
36 687 30.1 468 4 US-09-631-603-19 Sequence 19, Appl  
37 687 30.1 525 2 US-08-811-897A-23 Sequence 23, Appl  
38 687 30.1 525 2 US-08-855-213-23 Sequence 23, Appl  
39 687 30.1 525 3 US-09-201-474-23 Sequence 23, Appl  
40 684 30.0 448 2 US-08-811-897A-18 Sequence 18, Appl  
41 684 30.0 448 2 US-08-855-213-18 Sequence 18, Appl  
42 684 30.0 448 3 US-09-201-474-18 Sequence 18, Appl  
43 684 30.0 467 2 US-08-811-897A-19 Sequence 19, Appl  
44 684 30.0 467 2 US-08-855-213-19 Sequence 19, Appl  
45 684 30.0 467 3 US-09-201-474-19 Sequence 19, Appl

#### ALIGNMENTS

RESULT 1  
US-08-468-249A-20  
; Sequence 20, Application US/08468249A  
; Patent No. 5886148  
; GENERAL INFORMATION:  
; APPLICANT: Segre et al., Gino V.  
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA  
; TITLE OF INVENTION: ENCODING SAME  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/468,249A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/864,475  
; FILING DATE: 06-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/681,702  
; FILING DATE: 04-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Frazer, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00786/071003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 591 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-468-249A-20

Query Match 96.1%; Score 2195; DB 2; Length 591;  
Best Local Similarity 73.6%; Pred. No. 9.8e-210;  
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;

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RESULT 2
US-09-631-603-21
; Sequence 21, Application US/09631603
; Patent No. 6733990
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin R.
; APPLICANT: Lloyd, Clare
; APPLICANT: Welch, Nadine
; TITLE OF INVENTION: 15571, A No. 6733990el GPCR-like Molecule of the
; TITLE OF INVENTION: Secretin-Like Family and Uses Thereof
; FILE REFERENCE: 5800-48A
; CURRENT APPLICATION NUMBER: US/09/631,603
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/515,781
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/146,916
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-631-603-21

Query Match      88.0%; Score 2008; DB 4; Length 593;
Best Local Similarity 67.3%; Pred. No. 4.1e-191;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY      1  MGAARIAPSLAILCCPVLSSAYAL-----25
      1  MGTERTAPGLAIICCPVLSSAYALDADVMTKBCIOIFLLHRAOACEKRLKEVLQPPA 60

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RESULT 3
US-08-468-249A-21
; Sequence 21, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 75
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003

```

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-5070  
; TELEFAX: 617/542-8906  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 593 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-468-249A-21

Query Match 87.7%; Score 2002; DB 2; Length 593;  
Best Local Similarity 67.1%; Pred. No. 1.6e-190;  
Matches 398; Conservative 10; Mismatches 27; Indels 158; Gaps 3;  
  
QY 1 MGAARTAPSLALLCCPVLSAYAL----- 25  
Db 1 MGTARIAPGLALLCCPVLSAYALVDDVMTKEQIFLLHRAQAQCEKRLKEVLQRA 60  
QY 26 ----- 25  
Db 61 SIMESDKGWTASTSGKPKDKASKGLYPESBEDKEAPTGSRYRGRPCLPWDHILCWPL 120  
QY 26 ----- 25  
Db 121 GAPGEVAVPCPDYIVDFNHKHAYRCDRNGSWELVPGHNRTWANYSECVKPLTNETRE 180  
QY 26 -EVFRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNYYHMHMFLSFMLRAASIFVK 84  
Db 181 REVFRRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNYYHMHMFLSFMLRAVSIFVK 240  
QY 85 DAVLYSGFTLDBAERLITEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLYFLATNYWIL 144  
Db 241 DAVLYSGATLDBAERLITEELRAIAQAQPPPPATAAGVAGCRVAVTFEFLYFLATNYWIL 300  
QY 145 VEGLYLHSLIFMAFPSEKKYLMGFTIFGWLPAVFAVWVGVRAVLANTGCDLSSGHKK 204  
Db 301 VEGLYLHSLIFMAFPSEKKYLMGFTVFGWGLPAVFAVWVGVRAVLANTGCDLSSGNKK 360  
QY 205 WIIQVPIILASVVLNFIINIRVLATKLRNAGRCQTRQYRKLRLSTLVLPFGVH 264  
Db 361 WIIQVPIILASVVLNFIINIRVLATKLRNAGRCQTRQYRKLRLSTLVLPFGVH 420  
QY 265 YTVFMALPYTEVSGTLWQIQMHEMLFNSFQGFVAILIYFCNGEVQAEIKKSWSRWTIA 324  
Db 421 YIVFMATPYTEVSGTLWQIQMHEMLFNSFQGFVAILIYFCNGEVQAEIKKSWSRWTIA 480  
QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVPGRVGLPLSPRLPTATTNGHPQLPGHAKP 383  
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVPGRVGLPLSPRLPTATTNGHPQLPGHAKP 540  
QY 384 GAPATET-ETLPVTMAVPPKDDGFLNGSCGLDEBASGARPPPLIQEGWETVM 435  
Db 541 GTPALETLETPPAAWPKDDGFLNGSCGLDEBASGARPPPLIQEGWETVM 593

RESULT 4  
US-08-142-439A-6  
; Sequence 6, Application US/08142439A  
; Patent No. 5670360  
; GENERAL INFORMATION:  
; APPLICANT: Thorens, Bernard  
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1  
; NUMBER OF INVENTION: (GLP-1)  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: No. 56703600 No. 56703600disk of No. 56703600th America, Inc.  
; STREET: 405 Lexington Avenue, Suite 6400  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10174-6201  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/142,439A  
FILING DATE: 24-NOV-93  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DK 398/92  
FILING DATE: 25-MAR-92  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00697  
FILING DATE: 23-MAR-93  
ATTORNEY/AGENT INFORMATION:  
NAME: Harrington, James J.  
REGISTRATION NUMBER: 38,711  
REFERENCE/DOCKET NUMBER: 3756.204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 867 0123  
TELEFAX: 212 867 0298  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 585 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Didelphis virginiana  
US-08-142-439A-6

Query Match 74.9%; Score 1710; DB 1; Length 585;  
Best Local Similarity 80.2%; Pred. No. 1.9e-161;  
Matches 333; Conservative 27; Mismatches 42; Indels 13; Gaps 7;  
  
QY 26 EVFDRGLMIYTVGYSMSLASLTAVLILAYFRRLHCTRNYYHMHMFLSFMLRAASIFVKD 85  
Db 179 EVFDRGLMIYTVGYSISLGSITVAVLILGYFRRLHCTRNYYHMHMFLSFMLRAVSIFIKD 238  
QY 86 AVLXSGFTLDBAERLITEELHIIAQVPPPPAAAAGVAGCRVAVTFEFLYFLATNYWILV 145  
Db 239 AVLXSGVSTDEITERITEELRAFT-EPADKA-GFVGCRVAVTVFLYFLTNTNYWILV 295  
QY 146 EGLYLHSLIFMAFPSEKKYLMGFTIFGWLPAVFAVWVGVRAVLANTGCDLSSGHKKW 205  
Db 296 EGLYLHSLIFMAFPSEKKYLMGFTIFGWLPAVFAVWVGVRAVLANTGCDLSSGNKKW 355  
QY 206 IIOVPIILASVVLNFIINIRVLATKLRNAGRCQTRQYRKLRLSTLVLPFGVHY 265  
Db 356 IIOVPIILAAIVVNFIINIRVLATKLRNAGRCQTRQYRKLRLSTLVLPFGVHY 415  
QY 266 TVFMALPYTEVSGTLWQIQMHEMLFNSFQGFVAILIYFCNGEVQAEIKKSWSRWTIAL 325  
Db 416 IVFMATPYTEVSGTLWQIQMHEMLFNSFQGFVAILIYFCNGEVQAEIKKSWSRWTIAL 475  
QY 326 DFKRRKARSGSSSYSGPMVSHTSVTNVPGRVGLPLSPRLPP--ATTNGHSQLPGHAK 382  
Db 476 DFKRRKARSGSSSYSGPMVSHTSVTNVPGRVGLPLSPRLAPGAGASANGHHQLPGYVK 535  
QY 383 PGAPATETETLPVTMAVPP--KDDGFLNGSCGLDEBASGARPPPLIQEGWETVM 435  
Db 536 HG--SISENSLPSSGPEPGTKDDGLNG--SGLYEPMVGE-QPPPLLEEEERETVM 585

RESULT 5  
US-08-142-551B-125  
; Sequence 125, Application US/08142551B  
; Patent No. 5814603  
; GENERAL INFORMATION:  
; APPLICANT: Oldenburg, Kevin R.





Query Match 67.9%; Score 1551; DB 2; Length 515;  
Best Local Similarity 86.6%; Pred. No. 1.1e-145;  
Matches 291; Conservative 18; Mismatches 24; Indels 3; Gaps 2;  
QY 26 EVFDRGLMITYGVGSMASLAVAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVKD 85  
DB 179 EVFDRGLMITYGVGSMASLAVAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVKD 238  
QY 86 AVLYSGFTLDEARLTEREELHIIAQVPPPPAAAGVAGCRVAVTFPLFLATNYWILV 145  
DB 239 AVLYSGVSTDEIRITEREELRAFTE--PPADKA-GFVGCRVAVTFPLFLATNYWILV 295  
QY 146 EGLYHLSLIPMAFFSEKKYLWGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 205  
DB 296 EGLYHLSLIPMAFFSEKKYLWGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 355  
QY 206 IIOVPLASVVLNFIILNIIRVATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265  
DB 356 IIOVPLAAIVNFIILNIIRVATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 415  
QY 266 TVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVVAIYFCNGEVOAIEKRSWRWTAL 325  
DB 416 IVFMATPYTEVSGTLWQIOMHYEMLFNSFGQFFVVAIYFCNGEVOAIEKRSWRWTAL 475  
QY 326 DFKRKARSGSSSYGPMVSHTSVTNVGPRAGLSLP 361  
DB 476 DFKRKARSGSSSYGPMVSHTSVTNVGPRGWP 511

RESULT 9  
US-09-449-632-2  
; Sequence 2, Application US/09449632  
; Patent No. 6541220  
; GENERAL INFORMATION:  
; APPLICANT: Jppner, Harald  
; APPLICANT: Rubin, David A.  
; TITLE OF INVENTION: PTHIR and PTH3R Receptors, Methods and Uses Thereof  
; FILE REFERENCE: 0609.4740001/SRL/M-G  
; CURRENT APPLICATION NUMBER: US/09/449,632  
; PRIOR FILING DATE: 1999-11-30  
; PRIOR FILING DATE: 1998-11-30  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; TYPE: PRT  
; ORGANISM: zebrafish  
US-09-449-632-2  
Query Match 64.2%; Score 1465; DB 4; Length 536;  
Best Local Similarity 68.8%; Pred. No. 4.1e-137;  
Matches 284; Conservative 45; Mismatches 66; Indels 18; Gaps 4;  
QY 26 EVFDRGLMITYGVGSMASLAVAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVKD 85  
DB 139 EVFDRGLMITYGVGSMASLAVAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVKD 198  
QY 86 AVLYSGFTLDEARLTEREELHIIAQVPPPPAAAGVAGCRVAVTFPLFLATNYWILV 145  
DB 199 VLYSGSALQEWERTVEDLKSITEAPP--ANKTQIFGCKVAVTFPLFLATNYWILV 255  
QY 146 EGLYHLSLIPMAFFSEKKYLWGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 205  
DB 256 EGLYHLSLIPMAFFSEKKYLWGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 315  
QY 206 IIOVPLASVVLNFIILNIIRVATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265  
DB 316 IIOVPLAAIVNFIILNIIRVATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 375  
QY 266 TVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVVAIYFCNGEVOAIEKRSWRWTAL 325  
DB 376 IVFMATPYTEVSGTLWQIOMHYEMLFNSFGQFFVVAIYFCNGEVOAIEKRSWRWTAL 435

QY 326 DFKRKARSGSSSYGPMVSHTSVTNVGPRAGLSLPRLPPATNTHSHQSLPCHAKPGA 385  
DB 436 DFKRKARSGSSSYGPMVSHTSVTNVGPRAGLSLPRLPPATNTHSHQSLPCHAKPGA 495  
QY 386 PATETETLPTVWAPKDDGFLNGSCGLDBEASGSARPPPLQ---EGHETVM 435  
DB 496 VSEN-----SIPSSGHELHIQ-----EETPSKTFQMEKTIQVVEEBRETVM 536  
RESULT 10  
US-09-449-632-4  
; Sequence 4, Application US/09449632  
; Patent No. 6541220  
; GENERAL INFORMATION:  
; APPLICANT: Jppner, Harald  
; APPLICANT: Rubin, David A.  
; TITLE OF INVENTION: PTHIR and PTH3R Receptors, Methods and Uses Thereof  
; FILE REFERENCE: 0609.4740001/SRL/M-G  
; CURRENT APPLICATION NUMBER: US/09/449,632  
; CURRENT FILING DATE: 1999-11-30  
; PRIOR FILING DATE: 1998-11-30  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 542  
; TYPE: PRT  
; ORGANISM: zebrafish  
US-09-449-632-4  
Query Match 49.5%; Score 1130; DB 4; Length 542;  
Best Local Similarity 59.4%; Pred. No. 9.3e-104;  
Matches 230; Conservative 49; Mismatches 74; Indels 34; Gaps 7;  
QY 26 EVFDRGLMITYGVGSMASLAVAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVKD 85  
DB 136 EVFDRGLMITYGVGSMASLAVAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVKD 195  
QY 86 AVLYSGFTLDEARLTEREELHIIAQVPPPPAAAGVAGCRVAVTFPLFLATNYWILV 145  
DB 196 AVLYAVNDGELEDAVEQRPV-----GCKAAVTLFLYLLATNHYWILV 240  
QY 146 EGLYHLSLIPMAFFSEKKYLWGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 205  
DB 241 EGLYHLSLIPMAFFSEKKYLWGFTIFGWLPAFVAVVWVVRATLANTGCWDLSSGHKKW 300  
QY 206 IIOVPLASVVLNFIILNIIRVATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 265  
DB 301 IIOVPLAAIVNFIILNIIRVATKLRETNAGRCDTROQYRKLRLSTLVLPLFGVHY 360  
QY 266 TVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVVAIYFCNGEVOAIEKRSWRWTAL 325  
DB 361 MLFMALPYTDVIGLRLQILMHYEMLFNSQGFVAFYFCNGEVOAIEKRSWRWTAL 420  
QY 326 DFKRKAR-----SGSSSYGPMVSHTSVTNV-----GPRAGLSLPRLPPATNTHSHQ 376  
DB 421 DLKQKARVHSSAGCGSYGCGMHSHTTQSVCLSVSGAKGGHSL-----HTTGAQGGSHLQ 476  
QY 377 LPGHAKGAPATETETL---PVTMAVPK 401  
DB 477 HSGNL-PGYAPQDTETLFPV---VPK 499

RESULT 11  
US-09-449-632-5  
; Sequence 5, Application US/09449632  
; Patent No. 6541220  
; GENERAL INFORMATION:  
; APPLICANT: Jppner, Harald  
; APPLICANT: Rubin, David A.  
; TITLE OF INVENTION: PTHIR and PTH3R Receptors, Methods and Uses Thereof  
; FILE REFERENCE: 0609.4740001/SRL/M-G



; CURRENT APPLICATION NUMBER: US/09/449,632  
; CURRENT FILING DATE: 1999-11-30  
; PRIOR APPLICATION NUMBER: US 60/110,467  
; PRIOR FILING DATE: 1998-11-30  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: zebrafish  
US-09-449-632-5

Query Match 46.8%; Score 1068; DB 4; Length 575;  
Best Local Similarity 50.9%; Pred. No. 1-5e-97;  
Matches 215; Conservative 71; Mismatches 106; Indels 30; Gaps 8;  
QY 28 FORLGMITYVGYSMASLASLTAVLILAYFRRLHCTRNYYIHMMFLSFMLRAASIFVKDAV 87  
Db 169 FERLHIMTYGVAVSFSSLLVAIFIIIGYFRRLHCTRNYYIHMMFLFVSFMLRAASIFVKDHV 228  
QY 88 LYSGFTLDEAERLLEEELHIIAQVPPPPAAAVGAGCRVAVTFFLYFLATNYYWILVEG 147  
Db 229 VHTSAGLOESDAVLMNFTNAVDPVDSQ---YMGCKVTLLFFLYFLATNYYWILVEG 285  
QY 148 LYLHSLIFMAFPSEKKYLMGFTIFGMLPAVFAVAVVGVVAVRATLANTGCWDLSSGHKKWII 207  
Db 286 LYLHSLIFMAFLSDSKYLMGFTILGWGVPVAVFAVAVVAVRATLADARCHELSAGNIKWIY 345  
QY 208 QVPILASVNLFIINIRVATKLRETNAGCDTRQYRKLRLSTLVLPFGVHYTV 267  
Db 346 QEPILATGLNFIINIRVATKLRETNAGCDTRQYRKLRLSTLVLPFGVHYTV 405  
QY 268 FMALPTEVSGTLWQIOMHYEMLNSFGQFFVAILIYFCNCGEVOAEIRKSWRWTALDF 327  
Db 406 FVGMPT- FEGLGWEERMYCELFNFSQGFVSIILYICNCGEVOAEIRKSWRWTALDF 464  
QY 328 KRKARSSSSYSGPMV-----SHTSVTVNGPRAGLSPLSPRLPPA-----TTNGHS 375  
Db 465 KGPVVCGSN--RYGSLVTLGNSTSSQSLAAGGPGTSTTLFSSRVVRSOGPTVSTHA 522  
QY 376 QLPGHAKGAPATETETPLTVMAVPKDDGLNGSCGLDE---EASGSARPPLPQEGWE 432  
Db 523 TLPGVVL---NSDADSLPPSIPPEPED-----SAQVDDILLKESLPTPSSGLEDDDE 573  
QY 433 TV 434  
Db 574 TL 575

RESULT 12  
US-09-631-603-20  
; Sequence 20, Application US/09631603  
; Patent No. 6733990  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin R.  
; APPLICANT: Lloyd, Clare  
; APPLICANT: Weich, Nadine  
; TITLE OF INVENTION: 15571, A No. 6733990a1 GPCR-like Molecule of the  
; TITLE OF INVENTION: Secretin-like Family and Uses Thereof  
; FILE REFERENCE: 5800-48A  
; CURRENT APPLICATION NUMBER: US/09/631,603  
; CURRENT FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/515,781  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR APPLICATION NUMBER: 60/146,916  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 20  
; LENGTH: 550  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-631-603-20

Query Match 46.0%; Score 1050.5; DB 4; Length 550;  
Best Local Similarity 53.9%; Pred. No. 7.8e-96;  
Matches 208; Conservative 58; Mismatches 85; Indels 35; Gaps 7;  
QY 26 EVFDRLGMIYTVGYSMASLASLTAVLILAYFRRLHCTRNYYIHMMFLSFMLRAASIFVKD 85  
Db 139 EFFERLYVMYTVGYSGISFGSLAVAILIIGYFRRLHCTRNYYIHMMFLFVSFMLRATSIIFVKD 198  
QY 86 AVLYSGFTLDEAERLLEEELHIIAQVPPPPAAAVG-----YACRCVAVTFFLYFLATNY 140  
Db 199 RVVHAHIGVKELES-----IMDDPNQSIATSVDKSYIGCKIAVVMFYFLATNY 251  
QY 141 YWILVEGLYLHSLIFMAFPSEKKYLMGFTIFGMLPAVFAVAVVGVVAVRATLANTGCWDLSS 200  
Db 252 YWILVEGLYLHNLIFVAFESDTKYLWGFFPAAFVAAVAVARATLADARCHELSA 311  
QY 201 GHKKWIIQVPIILASVNLFIINIRVATKLRETNAGCDTRQYRKLRLSTLVLP 260  
Db 312 GDIKWIYQAPILAAIGLNFILNTRVRLATKIWETNAVGHDTKQYRKLAKSTLVLV 371  
QY 261 FGVHYTVFMALPTEVSGTLWQIOMHYEMLNSFGQFFVAILIYFCNCGEVOAEIRKSWR 320  
Db 372 FGVHYTVFVCLPHS-FTGLGWEIRHCELFNFSQGFVSIILYICNCGEVOAEIRKSWR 430  
QY 321 WTLALDFKREKARSGS-----SSSYSGPMVSHTSVTVNGPRAGLSPLSPRLPP 368  
Db 431 WNLSDVMKRTPCGSRRCGSLVTTVHTSTSSQSLAAGGPGTSTTLFSSRVVRSOGPTVSTHA 486  
QY 369 ATTNGHSQLPGHAKGAPATETETPLP 394  
Db 487 ---DSHTLPGYVWSN---SEODCLP 506

RESULT 13  
US-08-468-011A-2  
; Sequence 2, Application US/08468011A  
; Patent No. 6030804  
; GENERAL INFORMATION:  
; APPLICANT: Soppet, Daniel R  
; APPLICANT: Yi, Li  
; APPLICANT: Rosen, Craig A  
; APPLICANT: Ruben, Steven  
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor  
; TITLE OF INVENTION: HLTG74  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
; ADDRESSEE: Stewart & Olstein  
; STREET: 6 Becker Farm Road  
; CITY: Roseland  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07068-1739  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA: US/08/468,011A  
; APPLICATION NUMBER: US/08/468,011A  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 541 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-011A-2

Query Match 45.4%; Score 1036; DB 3; Length 541;  
Best Local Similarity 51.3%; Pred. No. 2.1e-94;  
Matches 214; Conservative 61; Mismatches 102; Indels 40; Gaps 8;

QY 26 EVFDRGLMITYGVYSGLASLTAVLILAYFRRLHCTRNIIHMHFLSFMLRAASIFVKD 85  
DB 139 EFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNIIHMHFLSFMLRATSIFVKD 198  
QY 86 AVLYSGFTLDEAERLTELHIIIAQVPPPPAAAAGV-----YAGCRVAVTFYFLATNY 140  
DB 199 RVVHAHIGVKELES-----IMQDDPQNSIEATSDVKSQYIGCKIAVVMFYFLATNY 251  
QY 141 YWILVEGLYLHSLIFWAFSEKKYLGWFTIFGWLPAFVAVVAVVAVRATLANTGCDLSS 200  
DB 252 YWILVEGLYLHNLIFVAFSDTKYLGWFTIFGWLPAFVAVVAVVAVRATLADARCWELSA 311  
QY 201 GHKKWIIQVPIIASVNLFINIIRVATKLRNAGRCDDTRQYRKLRLSTLVLP 260  
DB 312 GDKWIIQVPIIAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRKLAKSTLVLP 371  
QY 261 FGVIYTVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSR 320  
DB 372 FGVIYTVFVCLPHS-FTGLGWEIRMEHCELFNSFGQFFVSIYCYCNGEVOAEVKKWMSR 430  
QY 321 WTALDPKPKARSGSSSY-SYGPVMSHTSVTVNGPRAG---LSLPLSPRLPP---ATTN 372  
DB 431 WNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQSQVAAHAWCLSLAKLPRSPADSLTATS 490  
QY 373 GHSOLPGHAKPGAPATETETPLVTMAVPKDDGFLNGSCGLDEEASGARPPPLQ 429  
DB 491 LYLAMSG-----VTQRTASHTLSTRS-----NKEDSGRQDDILMEK 528

## RESULT 14

US-09-236-468A-2  
Sequence 2, Application US/09236468A  
Patent No. 6338951  
GENERAL INFORMATION:  
APPLICANT: Soppet et al.  
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDTG74  
FILE REFERENCE: P201D1  
CURRENT APPLICATION NUMBER: US/09/236,468A  
PRIOR FILING DATE: 1999-01-25  
PRIOR APPLICATION NUMBER: 08/468,011  
PRIOR FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 2  
LENGTH: 541  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-236-468A-2

Query Match 45.4%; Score 1036; DB 3; Length 541;  
Best Local Similarity 51.3%; Pred. No. 2.1e-94;  
Matches 214; Conservative 61; Mismatches 102; Indels 40; Gaps 8;

QY 26 EVFDRGLMITYGVYSGLASLTAVLILAYFRRLHCTRNIIHMHFLSFMLRAASIFVKD 85  
DB 139 EFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNIIHMHFLSFMLRATSIFVKD 198  
QY 86 AVLYSGFTLDEAERLTELHIIIAQVPPPPAAAAGV-----YAGCRVAVTFYFLATNY 140  
DB 199 RVVHAHIGVKELES-----IMQDDPQNSIEATSDVKSQYIGCKIAVVMFYFLATNY 251  
QY 141 YWILVEGLYLHSLIFWAFSEKKYLGWFTIFGWLPAFVAVVAVVAVRATLANTGCDLSS 200  
DB 252 YWILVEGLYLHNLIFVAFSDTKYLGWFTIFGWLPAFVAVVAVVAVRATLADARCWELSA 311

QY 201 GHKKWIIQVPIIASVNLFINIIRVATKLRNAGRCDDTRQYRKLRLSTLVLP 260  
DB 312 GDKWIIQVPIIAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRKLAKSTLVLP 371  
QY 261 FGVIYTVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAILIYFCNGEVOAEIRKWSR 320  
DB 372 FGVIYTVFVCLPHS-FTGLGWEIRMEHCELFNSFGQFFVSIYCYCNGEVOAEVKKWMSR 430  
QY 321 WTALDPKPKARSGSSSY-SYGPVMSHTSVTVNGPRAG---LSLPLSPRLPP---ATTN 372  
DB 431 WNLSDVMKRTPPCGSRRCGSLVTTVTHSTSSQSQVAAHAWCLSLAKLPRSPADSLTATS 490  
QY 373 GHSOLPGHAKPGAPATETETPLVTMAVPKDDGFLNGSCGLDEEASGARPPPLQ 429  
DB 491 LYLAMSG-----VTQRTASHTLSTRS-----NKEDSGRQDDILMEK 528

## RESULT 15

PCT-US95-07085-2  
Sequence 2, Application PC/TUS9507085  
GENERAL INFORMATION:  
APPLICANT: Soppet, Daniel R  
APPLICANT: Yi, Li  
APPLICANT: Rosen, Craig A  
APPLICANT: Ruben, Steven  
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor  
TITLE OF INVENTION: HLTDTG74  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,  
ADDRESS: Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: NJ  
COUNTRY: USA  
ZIP: 07068-1739  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/07085  
FILING DATE: 05-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-393  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 541 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-07085-2

Query Match 45.4%; Score 1036; DB 5; Length 541;  
Best Local Similarity 51.3%; Pred. No. 2.1e-94;  
Matches 214; Conservative 61; Mismatches 102; Indels 40; Gaps 8;

QY 26 EVFDRGLMITYGVYSGLASLTAVLILAYFRRLHCTRNIIHMHFLSFMLRAASIFVKD 85  
DB 139 EFCERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNIIHMHFLSFMLRATSIFVKD 198  
QY 86 AVLYSGFTLDEAERLTELHIIIAQVPPPPAAAAGV-----YAGCRVAVTFYFLATNY 140  
DB 199 RVVHAHIGVKELES-----IMQDDPQNSIEATSDVKSQYIGCKIAVVMFYFLATNY 251

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QY 141 YWILVEGLYLHSLIFMAFFSEKYLWGFTIFGWLPAFVAVWVGVYRATLANTGWDLSS 200
Db 252 YWILVEGLYLHSLIFMAFFSDTKYLWGFTILGWFPAFVAAWAVARATLADARCWELSA 311
QY 201 GHKKWIIQVPILASVVLNFIILFIRVLATKLRETNAGRCTRQOYRKLRLSTLVIVPL 260
Db 312 GDKIWIYOAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLAKSTLVIVLV 371
QY 261 FGVHYTVFWMALPYTEVSGTILWOIOMHYEMLFNSFQGFVVAIIYFCNGEVOAEIRKWSR 320
Db 372 FGVHYIVFVCLPHS-FIPLGWEIRMECELFNSFQGFVVAIIYFCNGEVOAEIRKWSR 430
QY 321 WTLALDFKRKARGSSSY-SYGPWVSHTSVTNVGPRAG-----LSLPLSPRLPP---ATTN 372
Db 431 WNLSDVDMKRTPPCGSRRCGSLVTTVTHSTSSQSOVAAAHAWCLSLAKLPRSPADSLTATS 490
QY 373 GHSQLPCHAKPGAPATETETLPTVMAVPKDDGFLNGSCGLDEEASGSARPPPLLOE 429
Db 491 LYLAMSG-----VTQSRASHTLSTRS-----NKEDSGRQRDDILMEK 528

```

Search completed: November 23, 2004, 21:00:18  
Job time : 42 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 23, 2004, 20:42:43 ; Search time 155 Seconds  
(without alignments)  
1006.756 Million cell updates/sec

Title: US-09-869-565-2

Perfect score: 2283

Sequence: 1 MGARIAPSLALLCCPVLS.....EASGSARPPPLQEGNETVM 435

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:.\*  
1: geneseq1980s:.\*  
2: geneseq1990s:.\*  
3: geneseq2000s:.\*  
4: geneseq2001s:.\*  
5: geneseq2002s:.\*  
6: geneseq2003as:.\*  
7: geneseq2003bs:.\*  
8: geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2283	100.0	435	3 AAB07529	AAB07529 A mutant
2	2264.5	99.2	446	3 AAY96983	AAY96983 Tethered
3	2195	96.1	591	2 AAR92277	AAR92277 Rat bone
4	2195	96.1	591	2 AAW73316	AAW73316 Parathyro
5	2195	96.1	591	8 ADH61247	ADH61247 Rat bone
6	2187	95.8	591	2 AAR27706	AAR27706 Rat bone
7	2187	95.8	591	7 ADE83416	ADE83416 Rat Prote
8	2146	94.0	591	8 ADO29629	ADO29629 Mouse GPC
9	2077.5	91.0	448	3 AAY96986	AAY96986 Human tet
10	2077	91.0	435	3 AAY96987	AAY96987 Human tet
11	2076.5	91.0	450	3 AAY96988	AAY96988 Human tet
12	2008	88.0	593	4 AAB71876	AAB71876 Human PTR
13	2008	88.0	593	6 AABP81872	AABP81872 Human par
14	2008	88.0	593	7 ADE83418	ADE83418 Human Pro
15	2008	88.0	593	7 ADF070390	ADF070390 Human PTH
16	2008	88.0	593	8 ADO29628	ADO29628 Human GPC
17	2008	88.0	593	8 ADQ18189	ADQ18189 Human sof
18	2008	88.0	593	8 ADO76825	ADO76825 Human wil
19	2002	87.7	593	2 AAW73317	AAW73317 Human par
20	2002	87.7	593	4 ABB56385	ABB56385 Non-endog
21	2002	87.7	593	8 ADH61248	ADH61248 Human PTH
22	1960	85.9	593	2 AAR92278	AAR92278 Human kid
23	1957	85.7	595	6 ABG73825	ABG73825 Canine pa
24	1862.5	81.6	614	2 AAR27707	AAR27707 Human kid
25	1710	74.9	585	2 AAR27705	AAR27705 Opossum k

26	1710	74.9	585	2 AAR92276	AAR92276 Opossum k
27	1710	74.9	585	2 AAW73315	AAW73315 Parathyro
28	1710	74.9	585	8 ADH61246	ADH61246 Opossum k
29	1698	74.4	964	7 ADC86169	ADC86169 Human GPC
30	1696	74.3	324	3 AAY96985	AAY96985 Tethered
31	1677.5	73.5	335	3 AAY96984	AAY96984 Tethered
32	1551	67.9	515	2 AAR92275	AAR92275 Opossum k
33	1551	67.9	515	2 AAW73314	AAW73314 Parathyro
34	1551	67.9	515	8 ADH61245	ADH61245 Opossum k
35	1538	67.4	515	2 AAR27704	AAR27704 Opossum k
36	1478	64.7	975	8 ADQ76835	ADQ76835 Parathyro
37	1465	64.2	536	3 AAY90230	AAY90230 Zebrafish
38	1465	64.2	536	3 AAY99600	AAY99600 Zebrafish
39	1465	64.2	536	7 ADC42305	ADC42305 Zebrafish
40	1465	64.2	536	7 ADH61059	ADH61059 Zebrafish
41	1151	50.4	542	3 AAY99601	AAY99601 Zebrafish
42	1130	49.5	542	7 ADC42307	ADC42307 Zebrafish
43	1130	49.5	542	7 ADH61061	ADH61061 Zebrafish
44	1122	49.1	523	3 AAY90231	AAY90231 Zebrafish
45	1068	46.8	575	7 ADC42308	ADC42308 Parathyro

## ALIGNMENTS

RESULT 1  
AAB07529  
ID AAB07529 standard; protein; 435 AA.  
XX  
AC AAB07529;  
XX  
DT 20-OCT-2000 (first entry)  
XX  
DE A mutant parathyroid hormone (PTH) receptor designated rdeltant.  
XX  
KW Mutant; parathyroid hormone; PTH; receptor; rdeltant;  
KW ligand binding domain.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
FT Peptide 1..22  
FT Protein /note= "signal peptide"  
FT Protein 23..435  
FT Protein /note= "mature protein"

PN WO200040698-A1.

PD 13-JUL-2000.

PF 31-DEC-1998; 98WO-US027862.

PR 31-DEC-1998; 98WO-US027862.

PA (GEHO ) GEN HOSPITAL CORP.

XX Gardella TJ, Kronenberg HM, Potts JT;

XX WPI; 2000-465971/40.

XX N-PSDB; AAA58932.

PT New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a deletion of the extracellular amino-terminus ligand binding domain, useful in screening assays for identifying agonists and antagonists of PTH receptor activity.

PS Claim 17; Fig 1; 81pp; English.

XX The present sequence represents a mutant parathyroid hormone (PTH) receptor, designated rdeltant. The polypeptide is characterised by a deletion of the extracellular amino-terminus ligand binding domain. The receptor has a minimal domain for ligand binding and is, therefore, useful in screening assays designed for the identification of agonists

CC and antagonists of PTH receptor activity

XX Sequence 435 AA;  
SQ  
Query Match 100.0%; Score 2283; DB 3; Length 435;  
Best Local Similarity 100.0%; Pred. No. 3.8e-217;  
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGAARIAPSLALLCCPVLSSAYALEVDFRLGMIYTVGYSMASLTVAVLILAYFRRLH 60  
Db 1 MGAARIAPSLALLCCPVLSSAYALEVDFRLGMIYTVGYSMASLTVAVLILAYFRRLH 60  
QY 61 CTRNYIHMFLSPMLRAASIFVKDAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAV 120  
Db 61 CTRNYIHMFLSPMLRAASIFVKDAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAV 120  
QY 121 GYACRVAVTFYFLYFLATNYWTLVEGLYLHSLIFMAFFSEKKYLMGFTIFGMLPAVFV 180  
Db 121 GYACRVAVTFYFLYFLATNYWTLVEGLYLHSLIFMAFFSEKKYLMGFTIFGMLPAVFV 180  
QY 181 AVWGVVRATLANTGCWDLSSGHKKWIIQVPIIASVVLNFIILINIRVLATKLRNAGR 240  
Db 181 AVWGVVRATLANTGCWDLSSGHKKWIIQVPIIASVVLNFIILINIRVLATKLRNAGR 240  
QY 241 CDRQYQYKRLRLTLLVPLFGVHYTVFMAIPYTVSGTLWQIQMHVEMLFNSFGPFVA 300  
Db 241 CDRQYQYKRLRLTLLVPLFGVHYTVFMAIPYTVSGTLWQIQMHVEMLFNSFGPFVA 300  
QY 301 ILYCFNGEYQAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 360  
Db 301 ILYCFNGEYQAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSVTNVGPRAGLSL 360  
QY 361 PLSPLPPATNGHSQLPGHAKPGAPATETETLPVTMAVPKDDGFLNGSCGLDEBASGS 420  
Db 361 PLSPLPPATNGHSQLPGHAKPGAPATETETLPVTMAVPKDDGFLNGSCGLDEBASGS 420  
QY 421 ARPPPLLOEGWETVM 435  
Db 421 ARPPPLLOEGWETVM 435

RESULT 2  
AAY96983  
ID AAY96983 standard; protein; 446 AA.

XX AAY96983;

XX 31-OCT-2000 (first entry)

DE Tethered PTH-1 receptor, Tether1.

XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.

XX Rattus sp.

OS Synthetic.

OS Chimeric.

XX Key Location/Qualifiers

FT Peptide 1..23

FT Peptide /label= PTH-1\_receptor\_signal\_sequence

FT Peptide 24..32

FT Peptide /label= PTH\_residues\_1-9

FT Peptide 33..36

FT Peptide /label= linker

FT Protein 37..446

FT Protein /label= PTH-1\_receptor

FT Protein /note= "residue 182 to end"

XX WO2000039278-A2.

XX 06-JUL-2000.

XX

PF 30-DEC-1999; 99WO-US031108.  
XX 31-DEC-1998; 98US-0114577P.  
XX  
PA (GARD/) GARDELLA T J.  
PA (KRON/) KRONENBERG H M.  
PA (POTT/) POTTS J T.  
PA (JUEP/) JUEPPNER H.  
XX  
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX WPI; 2000-452384/39.  
XX N-PSDB; AAA51732.  
XX  
XX New compound comprising an amino terminal signaling functional domain  
PT linked to a carboxy-terminal binding portion of parathyroid hormone for  
PT treating mammalian conditions characterized by decreases in bone mass.  
XX  
XX Claim 22; Fig 7; 119pp; English.  
XX  
XX Compounds of the structure or formula S-(L)-n-B, R-1-S-(L)-n-R or S-(L)-n  
-R, are new. S is an amino terminal signaling functional domain of  
XX parathyroid hormone (PTH); L is a linker molecule present n times (where  
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
XX portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R is the  
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
XX sequence. The new compounds are used for treating mammalian conditions  
XX characterized by decreases in bone mass, determining rates of bone  
XX reformation, bone resorption and/or bone remodeling, treating diseases  
XX and disorders associated with decreased tether activity, increasing CAMP  
XX in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
XX non-peptide PTH (claimed). The new compound can be administered by  
XX inhalation unlike the large native PTH or PTHrP which avoids the need for  
XX regular injections to treat osteoporosis  
SQ Sequence 446 AA;

Query Match 99.2%; Score 2264.5; DB 3; Length 446;  
Best Local Similarity 97.3%; Pred. No. 2.7e-215;  
Matches 434; Conservative 1; Mismatches 0; Indels 11; Gaps 1;

QY 1 MGAARIAPSLALLCCPVLSSAYAL-----EVFDRLGMIYTVGYSMASLTVA 49  
Db 1 MGAARIAPSLALLCCPVLSSAYAVSEIQLMHGGGGEVDFRLGMIYTVGYSMASLTVA 60  
QY 50 VLILAYFRRLHCTRNHYIHMFLSPMLRAASIFVKDAVLYSGFTLDEARLTTEELHIIA 109  
Db 61 VLILAYFRRLHCTRNHYIHMFLSPMLRAASIFVKDAVLYSGFTLDEARLTTEELHIIA 120  
QY 110 QVPPPPAAAAVGVAGCRVAVTFYFLYFLATNYWTLVEGLYLHSLIFMAFFSEKKYLMGFT 169  
Db 121 QVPPPPAAAAVGVAGCRVAVTFYFLYFLATNYWTLVEGLYLHSLIFMAFFSEKKYLMGFT 180  
QY 170 IFGMLPAVFVAVWGVVRATLANTGCWDLSSGHKKWIIQVPIIASVVLNFIILINIRVL 229  
Db 181 IFGMLPAVFVAVWGVVRATLANTGCWDLSSGHKKWIIQVPIIASVVLNFIILINIRVL 240  
QY 230 ATKLRNAGRCCTROQYKRLRLTLLVPLFGVHYTVFMAIPYTVSGTLWQIQMHVEM 289  
Db 241 ATKLRNAGRCCTROQYKRLRLTLLVPLFGVHYTVFMAIPYTVSGTLWQIQMHVEM 300  
QY 290 LFNSFQGFVVAIYFCNGEYQAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSV 349  
Db 301 LFNSFQGFVVAIYFCNGEYQAEIRKSWRWTALDFKPKARSGSSSYSGPMVSHTSV 360  
QY 350 TNVGPRAGLSLPLSPRLPPATNGHSQLPGHAKPGAPATETETLPVTMAVPKDDGFLNGS 409  
Db 361 TNVGPRAGLSLPLSPRLPPATNGHSQLPGHAKPGAPATETETLPVTMAVPKDDGFLNGS 420  
QY 410 CSGLDEEASGSARPPPLLOEGWETVM 435  
Db 421 CSGLDEEASGSARPPPLLOEGWETVM 446



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XX PD 24-NOV-1998.
XX PF
XX XX
XX 06-JUN-1995; 95US-00471494.
XX 05-APR-1991; 91US-00681702.
XX 06-APR-1992; 92US-00864475.
XX (GEO ) GEN HOSPITAL CORP.
XX PA
XX PI Abou-Samra A, Juppner H, Potts JT, Segre GV, Schipani E;
XX PI Kronenberg HM;
XX XX
XX DR WPI; 1999-034124/03.
XX DR N-PSDB; AAU08390.
XX XX
XX PT Antibody to parathyroid hormone receptor - for diagnostic or therapeutic
XX PT use.
XX PS
XX PS Claim 6; Fig 3; 63pp; English.
XX CC
XX CC This sequence represents the rat parathyroid hormone (PTH) receptor R15B,
XX CC which is targeted by the antibody of the invention. The antibody of the
XX CC invention is immunoreactive with naturally occurring human, rat or
XX CC opossum PTH receptor. The antibody is useful for treating disorders
XX CC characterised by overstimulation of PTH receptors by their ligand and for
XX CC the diagnosis of PTH-related hypercalcaemia
XX XX
XX SQ Sequence 591 AA;
Query Match 96.1%; Score 2195; DB 2; Length 591;
Best Local Similarity 73.6%; Pred. No. 3.1e-208;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;
QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSAYALVDADDVFTKEQIIFLLHRAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTPTASTGKPKREKASKGKYPESKENKDVTGSRRRGRPCLPEDNDIVCWEL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCDYIYDFNHKGHAYRCDBNGSWEVVPCHNRTWANSCLFPMNTEKE 180
QY 26 -EVFRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRTNYIHMFMFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMSLASLTVAVLILAYFRRLHCTRTNYIHMFMFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAGVAGCVAVNTFFLYFLATNYWTL 144
Db 241 DAVLYSGFTLDEAERLTEELHIIAQVPPPPAAAGVAGCVAVNTFFLYFLATNYWTL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLGPFAVFAVWVGVRAVLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLGPFAVFAVWVGVRAVLANTGCDLSSGHKK 360
QY 205 WIIQVPIIASVNLNFIINIRVLATKLRETNAGCDTQOQVKLLRSTLVLPFGVH 264
Db 361 WIIQVPIIASVNLNFIINIRVLATKLRETNAGCDTQOQVKLLRSTLVLPFGVH 420
QY 265 YTVFMALPVTESGTLWQIOMHYEMLFNSFQGFVAILYFCNGEVOAIRKSWSRWTLA 324
Db 421 YTVFMALPVTESGTLWQIOMHYEMLFNSFQGFVAILYFCNGEVOAIRKSWSRWTLA 480
QY 325 LDFKKARSGSSSYSGPWSVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 384
Db 481 LDFKKARSGSSSYSGPWSVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPGHAKPG 540
QY 385 APATETETLPVTMAVPKDDGFLNGSCSLDDEASGASRPPPLQEGWETVM 435
Db 541 APATETETLPVTMAVPKDDGFLNGSCSLDDEASGASRPPPLQEGWETVM 591
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```
RESULT 5
ADH61247
ID ADH61247 standard; protein; 591 AA.
XX AC
XX ADH61247;
XX XX
XX 25-MAR-2004 (first entry)
XX DT
XX DE Rat bone PTH/PTHrP receptor, R15B.
XX XX
XX KW osteopathic; Parathyroid hormone receptor; hypercalcaemia;
XX KW hyperparathyroidism; osteoporosis; carcinoma; epidermoid cancer;
XX KW oesophagus multiple myeloma; hypocalcaemia; cytostatic; rat; PTH; PTHrP;
XX KW PTH-related protein; receptor.
XX XX
XX OS Rattus rattus.
XX XX
XX PH Key Location/Qualifiers
XX FT Region 193..211
XX FT /note= "Transmembrane region 1"
XX FT Region 222..240
XX FT /note= "Transmembrane region 2"
XX FT Region 300..315
XX FT /note= "Transmembrane region 3"
XX FT Region 326..342
XX FT /note= "Transmembrane region 4"
XX FT Region 365..383
XX FT /note= "Transmembrane region 5"
XX FT Region 409..428
XX FT /note= "Transmembrane region 6"
XX FT Region 445..463
XX FT /note= "Transmembrane region 7"
XX XX
XX US2003153041-A1.
XX PN
XX PD 14-AUG-2003.
XX XX
XX PF 09-OCT-2002; 2002US-00267730.
XX PR 05-APR-1991; 91US-00681702.
XX PR 06-APR-1992; 92US-00864475.
XX PR 06-JUN-1995; 95US-00471494.
XX PR 24-NOV-1998; 98US-00199874.
XX XX
XX PA (GEO ) GEN HOSPITAL CORP.
XX XX
XX PI Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
XX PI Schipani E;
XX XX
XX DR WPI; 2004-051107/05.
XX DR N-PSDB; ADH61258.
XX XX
XX PT New isolated DNA encoding parathyroid hormone receptor polypeptides,
XX PT useful for diagnosing and treating disorders associated with parathyroid
XX PT hormone receptors, e.g. hypercalcaemia, osteoporosis or multiple myeloma.
XX XX
XX PS Disclosure; SEQ ID NO 20; 71pp; English.
XX XX
XX CC The invention relates to parathyroid hormone (PTH) receptor and its
XX CC corresponding nucleic acid sequence. The parathyroid hormone receptor
XX CC polypeptides, polynucleotides and antibodies are useful for diagnosing,
XX CC prognosticating and treating disorders associated with parathyroid
XX CC hormone receptors, e.g. hypercalcaemia, hyperparathyroidism,
XX CC osteoporosis, carcinomas of the breast, lung and prostate, epidermoid
XX CC cancers of the head and neck of the oesophagus, multiple myeloma, or
XX CC hypercalcaemia. The DNAs and polypeptides are also useful for screening
XX CC candidate compounds for antagonistic or agonistic effects on parathyroid
XX CC hormone receptor activity. The compounds are also useful in manufacturing
XX CC diagnostic agents used as diagnostic tools to diagnose hypercalcaemia and
XX CC to distinguish between hypercalcaemic conditions. The present sequence is
XX CC rat bone PTH/PTHrP (PTH-related protein) receptor protein.
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```

XX SQ Sequence 591 AA;
Query Match
Best Local Similarity 96.1%; Score 2195; DB 8; Length 591;
Matches 435; Conservative 0; Mismatches 0; Indels 156; Gaps 1;

QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSAYALVDDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTASTSGKPRKEKASGFYKESKENDVPTGSRRRGRPCLPEDWNTVCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIDFNHKGHAYRRCDRNGSWEVPGHNRTWANYSECLKFMETRE 180
QY 26 -EVFDRLGMIYTVGYSMASLTAVALLAYFRRLHCTRNTHMHMFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMASLTAVALLAYFRRLHCTRNTHMHMFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYWTL 144
Db 241 DAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYWTL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFVAVVGVVAVVVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFVAVVGVVAVVVRATLANTGCDLSSGHKK 360
QY 205 WIIQVPIILASVNLFINIIRVLTATKLRETNAGRCDTROQYRKLRLSTVLVPLFGVH 264
Db 361 WIIQVPIILASVNLFINIIRVLTATKLRETNAGRCDTROQYRKLRLSTVLVPLFGVH 420
QY 265 YTFWALPYTEVSGTLWQIQMHEMLFNSFGFFVAILIYFCNGEVOAEIRKSWSRWTLA 324
Db 421 YTFWALPYTEVSGTLWQIQMHEMLFNSFGFFVAILIYFCNGEVOAEIRKSWSRWTLA 480
QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPRLPATTNGHSQLPCHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPRLPATTNGHSQLPCHAKPG 540
QY 385 APATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 435
Db 541 APATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 591

RESULT 6
AAR27706
ID AAR27706 standard; protein; 591 AA.
XX AC AAR27706;
XX AC AAR27706;
DT 25-MAR-2003 (revised)
DT 16-MAR-1993 (first entry)
XX XX
DE Rat bone PTH/PTHrP receptor clone R15B prod.
XX Parathyroid hormone; related protein; calcium; antagonist; antibodies;
KW hypercalcaemia.
XX Rattus rattus.
OS
XX WO9217602-A1.
XX
PD 15-OCT-1992.
XX
PF 06-APR-1992; 92WO-US002821.
XX
PR 05-APR-1991; 91US-00681702.
XX
PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

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XX PI Segre GV, Kronenberg HM, Abou-Samra A, Juppner H, Potts JT;
XX Schipani E;
DR WPI: 1992-366271/44.
DR N-PSDB; AAQ29606.
XX
PT New DNA encoding parathyroid hormone receptor, DNA and antibodies - for
PT (differential) diagnosis of hypercalcaemia, and diagnosis and treatment
PT of tumours.
XX
PS Claim 20; Fig 3; 91pp; English.
XX
CC The rat bone parathyroid hormone/parathyroid hormone related protein
CC (PTH/PTHrP) receptor protein sequence was deduced from clone R15B obtd.
CC by screening a rat osteosarcoma (ROS) cell cDNA library to isolate those
CC expressing functionally intact PTH/PTHrP receptor proteins, performed
CC according to Gearing et al., (EMBO J. 8: 3676, 1989), by identifying
CC colonies capable of binding a suitable radio- labelled ligand. The
CC protein may be used in a therapeutic compsn. to inhibit activation of PTH
CC or PTHrP and thus reduce the level of calcium in the blood. Cpd. capable
CC of competing with PTH or PTHrP for binding can be identified using the
CC protein and DNAs homologous to PTH DNA can be identified using fragments
CC of the clone as probes. The sequence may be used for the prodn. of
CC antibodies useful for the treatment, classification, prognosis and/or
CC treatment of disorders related to the interaction between a cell receptor
CC and a ligand such as in hypercalcaemia. See also AAR27704-16. (Updated on
CC 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 591 AA;
Query Match 95.8%; Score 2187; DB 2; Length 591;
Best Local Similarity 73.4%; Pred. No. 1.9e-207;
Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;

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QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25
Db 1 MGAARIAPSLALLCCPVLSAYALVDDVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA 60
QY 26 ----- 25
Db 61 NIMESDKGWTASTSGKPRKEKASGFYKESKENDVPTGSRRRGRPCLPEDWNTVCWPL 120
QY 26 ----- 25
Db 121 GAPGEVAVPCPDYIDFNHKGHAYRRCDRNGSWEVPGHNRTWANYSECLKFMETRE 180
QY 26 -EVFDRLGMIYTVGYSMASLTAVALLAYFRRLHCTRNTHMHMFLSFMLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSMASLTAVALLAYFRRLHCTRNTHMHMFLSFMLRAASIFVK 240
QY 85 DAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYWTL 144
Db 241 DAVLYSGFTLDEARLTTEELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYWTL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFVAVVGVVAVVVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWLPAVFVAVVGVVAVVVRATLANTGCDLSSGHKK 360
QY 205 WIIQVPIILASVNLFINIIRVLTATKLRETNAGRCDTROQYRKLRLSTVLVPLFGVH 264
Db 361 WIIQVPIILASVNLFINIIRVLTATKLRETNAGRCDTROQYRKLRLSTVLVPLFGVH 420
QY 265 YTFWALPYTEVSGTLWQIQMHEMLFNSFGFFVAILIYFCNGEVOAEIRKSWSRWTLA 324
Db 421 YTFWALPYTEVSGTLWQIQMHEMLFNSFGFFVAILIYFCNGEVOAEIRKSWSRWTLA 480
QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPRLPATTNGHSQLPCHAKPG 384
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSPLSPRLPATTNGHSQLPCHAKPG 540
QY 385 APATETETLPVTMAVPKDDGFLNGSCGLDEASGSARPPPLLOEGWETVM 435

```

Db 541 APATETPLVTWAVPKDDGFLNGSCGLDEASGSARPPPLQEGWETVM 591

RESULT 7  
ADE83416  
ID ADE83416 standard; protein; 591 AA.  
XX  
AC ADE83416;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Rat Protein P25961, SEQ ID NO 11011.  
XX  
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
OS Rattus norvegicus.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEMO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
PR WPI; 2003-268312/26.  
DR GENBANK; P25961.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC pain and a pharmaceutical composition comprising the one or more  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 591 AA;

Query Match 95.8%; Score 2187; DB 7; Length 591;  
Best Local Similarity 73.4%; Pred. No. 1.9e-207;

Matches 434; Conservative 0; Mismatches 1; Indels 156; Gaps 1;  
QY 1 MGAARTAPSLALILCCPVLSSAYAL----- 25  
Db 1 MGAARTAPSLALILCCPVLSSAYALVDADVFTEKBOIFLLHRAQAQCKLLKEVLHTAA 60  
QY 26 ----- 25  
Db 61 NIMESDKGWTPTASTSGKPRKEKASGKYPESKENKDVPTGSRRRGRFCLPEWDNIWCPL 120  
QY 26 ----- 25  
Db 121 GAPCEVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHNRTWANYSECLKFMETRE 180  
QY 26 -EYFDRLGMIYTVGYSNLSASLTVAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVK 84  
Db 181 REVFDRLGMIYTVGYSNLSASLTVAVLILAYFRRLHCTRNVIHMHMFLSFMRLAASIFVK 240  
QY 85 DAVLYSGFTLDEAERLTEEBELHIIAQVPPPPAAAAAGYAGCRVAVTFFLYFLATNYWIL 144  
Db 241 DAVLYSGFTLDEAERLTEEBELHIIAQVPPPPAAAAAGYAGCRVAVTFFLYFLATNYWIL 300  
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVWVGVTRATLANTGCDLSSGHKK 204  
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVWVGVTRATLANTGCDLSSGHKK 360  
QY 205 WIIQVPLASVNLNFIINIRVLATKLRETNAGCDTRQOYRKLRLSTLVLPLFGVH 264  
Db 361 WIIQVPLASVNLNFIINIRVLATKLRETNAGCDTRQOYRKLRLSTLVLPLFGVH 420  
QY 265 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAIYFCNGEVOAEIRKSRWTLA 324  
Db 421 YTVFMALPYTEVSGTLWQIOMHYEMLFNSFGQFFVAIYFCNGEVOAEIRKSRWTLA 480  
QY 325 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPG 384  
Db 481 LDFKRRKARSGSSSYSGPMVSHTSVTNVGPRAGLSLPLSPRLPATTNGHSQLPCHAKPG 540  
QY 385 APATETPLVTWAVPKDDGFLNGSCGLDEASGSARPPPLQEGWETVM 435  
Db 541 APATETPLVTWAVPKDDGFLNGSCGLDEASGSARPPPLQEGWETVM 591

RESULT 8  
ADO29629  
ID ADO29629 standard; protein; 591 AA.  
XX  
AC ADO29629;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Mouse GPCR PTHR1, SEQ ID NO:731.  
XX  
KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;  
KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
KW virucide; hepatotropic; antibacterial; antianemic; antiseborrheic;  
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
XX murine; receptor.  
XX  
OS Mus musculus.  
XX  
PN WO2004040000-A2.  
XX

PD 13-MAY-2004.  
 XX 09-SEP-2003; 2003WO-US028226.  
 XX 09-SEP-2002; 2002US-0409303P.  
 PR 09-APR-2003; 2003US-0461329P.  
 XX (PRIM-) PRIMAL INC.  
 PA Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
 PI Madisen L, McIlwain KL, Pavlova MN, Vaasilatis D, Zeng H;  
 XX N-PSDB; ADO30323.  
 DR WPI; 2004-390329/36.  
 DR N-PSDB; ADO30323.  
 XX Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX Claim 151; SEQ ID NO 731; 542pp; English.  
 PS The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridise to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
 CC invention. Note: The full sequence data for this patent did not form part  
 CC of the printed specification; those sequences not shown were obtained in  
 CC electronic format directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.  
 SQ Sequence 591 AA;  
 Query Match 94.0%; Score 2146; DB 8; Length 591;  
 Best Local Similarity 72.1%; Pred. No. 2.2e-203;  
 Matches 426; Conservative 2; Mismatches 7; Indels 156; Gaps 1;  
 QY 1 MGAARIAPSLALLCCPVLSAYAL----- 25  
 DB 1 MGTARIAPSLALLCCPVLSAYALVDADVFTKEEQIFLLHRAQAQCDKLLKEVLHTAA 60  
 QY 26 ----- 25  
 DB 61 NIMESDKWTDPASTSGKPRKEKPGKFPESKENKDVPTGSRGRGRCPLPEWDNIVCWPL 120  
 QY 26 ----- 25  
 DB 121 GAGEVVAVPCFDYIDFNHKGHAYRCDRNGSWEVFGHNRTWANYSECLKFMFTNETRE 180  
 QY 26 -EVPDLGLMIYTVGYSMASLSTVAVLILAYFRLLHCTRTNYIHMHFLSFMRAASIFVK 84

DB 181 REVFDRLGMIYTVGYSMASLSTVAVLILAYFRLLHCTRTNYIHMHFLSFMRAASIFVK 240  
 QY 85 DAVLYSGFTLDBAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFELYFLATNYWIL 144  
 DB 241 DAVLYSGFTLDBAERLTEELHIIAQVPPPPAAAAGVAGCRVAVTFELYFLATNYWIL 300  
 QY 145 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVWVGVVRATLANTGCDLSSGHKK 204  
 DB 301 VEGLYLHSLIFMAFFSEKKYLMGFTIFGWGLPAVFAVWVGVVRATLANTGCDLSSGHKK 360  
 QY 205 WIIQVPILASVNLFILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVH 264  
 DB 361 WIIQVPILASVNLFILFINIRVLATKLRETNAGRCDTROQYRKLRLSTLVLPFGVH 420  
 QY 265 YTVFVALPYEVSGLTQIOMHYEMLFNSFGFFVAILIYFCNGEVOAERKSWSRWTLA 324  
 DB 421 YTVFVALPYEVSGLTQIOMHYEMLFNSFGFFVAILIYFCNGEVOAERKSWSRWTLA 480  
 QY 325 LDFKFKARSGSSSYSGPMVSHSTVNTVGPAGLSLPLSPRLPPATNGHSQLPGHAKPG 384  
 DB 481 LDFKFKARSGSSSYSGPMVSHSTVNTVGPAGLSLPLSPRLPPATNGHSQLPGHAKPG 540  
 QY 385 APATETELPVTMAYPKDDGFLNGSCGLDEASGSARPPPLQEGWETVM 435  
 DB 541 APAIENETIPVTMTPVKDDGFLNGSCGLDEASGSARPPPLQEGWETVM 591  
 RESULT 9  
 AAY96986  
 ID AAY96986 standard; protein; 448 AA.  
 XX AAY96986;  
 AC AAY96986;  
 XX 31-OCT-2000 (first entry)  
 DT Human tethered PTH-1 receptor, Tether1.  
 XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
 KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.  
 OS Homo sapiens.  
 OS Synthetic.  
 OS Chimeric.  
 XX Key Location/Qualifiers  
 FT Peptide 1..23  
 FT /label= Signal sequence  
 FT /note= "Human PTH-1 receptor residues 1-23"  
 FT 24..32  
 FT /label= PTH(1-9)  
 FT 33..36  
 FT /label= Linker  
 FT Protein 37..448  
 FT /label= PTH-1 receptor  
 FT /note= "Human PTH-1 receptor residues 182-593"  
 XX WO200039278-A2.  
 XX 06-JUL-2000.  
 XX 30-DEC-1999; 99WO-US031108.  
 XX 31-DEC-1998; 98US-0114577P.  
 XX (GARD/) GARDELLA T J.  
 XX (KRON/) KRONENBERG H M.  
 XX (POTT/) POTTS J T.  
 XX (JUEP/) JUEPNER H.  
 XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
 XX WPI; 2000-452384/39.



Db 299 ILYFCNGEYQAEIKKSWSEWTLALDFKRSKSSSSSYGPMVSHTSVTNVCPRVLGL 358  
QY 361 PLSPR-LPATNTHGSHQHPGAPATET-ETLPVTMAVPKDDGFLNGSCSGLDEEAS 418  
Db 359 PUSPRLLPATNTHGSHQHPGAPATET-ETLPVTMAVPKDDGFLNGSCSGLDEEAS 418  
QY 419 GSARPPPLQEGWETVM 435  
Db 419 GPERPALLQEEWETVM 435

RESULT 11  
AA96988  
ID AA96988 standard; protein; 450 AA.  
AC AA96988;  
XX  
XX 31-OCT-2000 (first entry)  
DE Human tethered PTH-1 receptor, Tether-R11.  
KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;  
KW PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
OS Chimeric.  
XX  
FH Key  
FT Peptide  
FT 1. .23  
FT /label= Signal sequence  
FT /note= "Human PTH-1 receptor residues 1-23"  
FT Peptide  
FT 24. 34  
FT /label= PTH (1-11)  
FT Peptide  
FT 35. 38  
FT /label= Linker  
FT Protein  
FT 39. 450  
FT /label= PTH-1 receptor  
FT /note= "Human PTH-1 receptor residues 182-593"  
XX  
PN WO200039278-A2.  
XX  
XX 06-JUL-2000.  
XX 30-DEC-1999; 99WO-US031108.  
XX 31-DEC-1998; 98US-0114577P.  
XX (GARD//) GARDELLA T J.  
XX (KRON//) KRONENBERG H M.  
XX (POTT//) POTTS J T.  
XX (JUEP//) JUEPPNER H.  
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;  
XX WPI; 2000-452384/39.  
XX N-PSDB; AAA51737.  
XX  
XX New compound comprising an amino terminal signaling functional domain  
XX linked to a carboxy-terminal binding portion of parathyroid hormone for  
XX treating mammalian conditions characterized by decreases in bone mass.  
XX  
XX Example 4; Fig 19; 119pp; English.  
XX  
XX Compounds of the structure or formula S-(L) n-B, R 1-S-(L) n-R or S-(L) n  
XX -R, are new. S is an amino terminal signaling functional domain of  
XX parathyroid hormone (PTH); L is a linker molecule present n times (where  
XX n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding  
XX portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34); R 1 is the  
XX PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor  
XX sequence. The new compounds are used for treating mammalian conditions  
XX characterized by decreases in bone mass, determining rates of bone  
XX reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased tether1 activity, increasing CAMP  
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or  
CC non-peptide PTH (claimed). The new compound can be administered by  
CC inhalation unlike the large native PTH or PTHrP which avoids the need for  
CC regular injections to treat osteoporosis  
XX  
SQ Sequence 450 AA;  
Query Match 91.0%; Score 2076.5; DB 3; Length 450;  
Best Local Similarity 88.4%; Pred. No. 1.2e-196;  
Matches 398; Conservative 11; Mismatches 26; Indels 15; Gaps 3;  
QY 1 MGAARIAPSLALLCCPVLSAYAL-----EVFDRLGMIVTVGYSMASLASLT 47  
Db 1 MGTARIAPGLALLCCPVLSAYAVSEIQIMHNRGGGEVDFRLGMIYTVGYSVLSASLT 60  
QY 48 VAVLLIAYFRRLLHCTRNIIHMFELSFMLRAASIFVKDAVLYSGFTLDEARLTTELHI 107  
Db 61 VAVLLIAYFRRLLHCTRNIIHMFELSFMLRAASIFVKDAVLYSGATLDEARLTTELRA 120  
QY 108 IAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWG 167  
Db 121 IAQAPPPATAAGVAGCRVAVTFFLYFLATNYYWILVEGLYHLSLIFMAFFSEKKYLWG 180  
QY 168 FTIFGWLPAVFAVWVGVRAVLANTGCDLSSGHKKWIIQVPILASVVLNFIINIR 227  
Db 181 FTVFGWLPAVFAVWVSVRAVLANTGCDLSSGNKKWIIQVPILASVVLNFIINIR 240  
QY 228 VLATKLRETNACRCDTQOYRKLRLSTLVLPFGVHYTVFVALPYTEVSGTLWQIMHY 287  
Db 241 VLATKLRETNACRCDTQOYRKLRLSTLVLPFGVHYTVFVALPYTEVSGTLWQIMHY 300  
QY 288 EMLFNSFQGFVAILIYFCNGEYQAEIKKSWSEWTLALDFKRSKSSSSSYGPMVSH 347  
Db 301 EMLFNSFQGFVAILIYFCNGEYQAEIKKSWSEWTLALDFKRSKSSSSSYGPMVSH 360  
QY 348 SVTNVGRVGLPLSPRLPTATTNGHPQLFGHAKPGTFALETLETPPPAAAKDDGF 405  
Db 361 SVTNVGRVGLPLSPRLPTATTNGHPQLFGHAKPGTFALETLETPPPAAAKDDGF 420  
QY 406 LMGSCGLDEEASGSRPPPLLOEWETVM 435  
Db 421 LMGSCGLDEEASGSRPPPLLOEWETVM 450

RESULT 12  
AAB71876  
ID AAB71876 standard; protein; 593 AA.  
AC AAB71876;  
XX  
XX 03-MAY-2001 (first entry)  
XX Human PTHR seven transmembrane domain.  
XX  
XX Human; parathyroid hormone/parathyroid hormone-related peptide receptor;  
XX PTHR; h15571; immunomodulatory; vascular; hepatic; antiaethma;  
XX antimicrobial; antinflammatory; immunosuppressive; gene therapy;  
XX vaccine; G-protein coupled receptor; GPCR; liver fibrosis;  
XX respiratory disorder; infection; chronic inflammatory disease;  
XX organ-specific autoimmunity; graft rejection; cystic fibrosis.  
XX  
XX Homo sapiens.  
XX  
XX WO200109328-A1.  
XX  
XX 08-FEB-2001.  
XX  
XX 03-AUG-2000; 2000WO-US021278.  
XX  
XX 03-AUG-1999; 99US-0146916P.  
XX 29-FEB-2000; 2000US-00515781.

0537965

PA (MILL-) MILLENNIUM PHARM INC.  
XX Hodge MR, Lloyd C, Weich NS;  
XX WPI; 2001-138653/14.  
XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful  
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma.  
XX  
XX Disclosure; Fig 2; 145pp; English.  
XX  
XX The present sequence is a human G-protein coupled receptor (GPCR) used  
CC for comparison with the seven transmembrane domain of a novel GPCR  
CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be  
CC used in the prevention, treatment and diagnosis of diseases associated  
CC with inappropriate GPCR expression. Such diseases include immune,  
CC haematological, fibrotic, hepatic and respiratory disorders including  
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic  
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,  
CC graft rejection, graft versus host disease, cystic fibrosis and, in  
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens  
CC in the production of antibodies against GPCR and in assays to identify  
CC modulators (agonists and antagonists) of GPCR expression and activity.  
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down  
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be  
CC used as diagnostic agents for detecting the presence of GPCR polypeptides  
CC in samples  
XX  
SQ Sequence 593 AA;  
  
Query Match 88.0%; Score 2008; DB 4; Length 593;  
Best Local Similarity 67.3%; Pred. No. 1.1e-189;  
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;  
  
Qy 1 MGAARIAPSLALLCCPVLSSAYAL----- 25  
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKEEQIFLLHRAQAQCEKRLKVLQKPA 60  
Qy 26 ----- 25  
Db 61 SIMESDKGWTSASTSGKPRKDKASGLYPESEEDKEAPTGSRYGRPCLPEDWHILCWPL 120  
Qy 26 ----- 25  
Db 121 GAPEVVAVPCDDIYFENKHCHAYRCDRNGSWELVPGHNRWTWANYSECVKLTNETRE 180  
Qy 26 -EVEDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRTNYTHMHMFLSFMRLAASIFVK 84  
Db 181 REVDFRLGMIYTVGYSVSLASTVAVLILAYFRRLHCTRTNYTHMHFLSFMRLAASIFVK 240  
Qy 85 DAVLYSGFTLDEAERLFEELHIIAQQPPPAAGVAGCRVATFFLYFLATNYWIL 144  
Db 241 DAVLYSGATLDEAERLFEELRAIAQAAPPATAAAGVAGCRVATFFLYFLATNYWIL 300  
Qy 145 VEGLYLHSLIPWAFSEKKYLGWFTIFGWLPAVFAVAVVGVRAFLANTGCDLSSGHK 204  
Db 301 VEGLYLHSLIPWAFSEKKYLGWFTIFGWLPAVFAVAVVGVRAFLANTGCDLSSGNK 360  
Qy 205 WIIQVPIIASVVLNFIPIRVLATKLRETNACRCDTROQYRKLKSLTIVLPLFGVH 264  
Db 361 WIIQVPIIASVVLNFIPIRVLATKLRETNACRCDTROQYRKLKSLTIVLPLFGVH 420  
Qy 265 YTFVNLBYTEVSGTLQWQIOMHYEMLFNSFGFFVAILYFCNGEVRQAEIKKSWRWTLA 324  
Db 421 YIVFNLATYTEVSGTLQWQIOMHYEMLFNSFGFFVAILYFCNGEVRQAEIKKSWRWTLA 480  
Qy 325 LDFKFKARSGSSSYGPMWHSHTSVTVNGPRAGLSLPLSPR-LPPATNGHSQLPGHAKP 383  
Db 481 LDFKFKARSGSSSYGPMWHSHTSVTVNGPRVGLGLPLSPRLLPATTNGHSQLPGHAKP 540  
Qy 384 GAPATET-ETLFTVWAVPKDDGFLNGSCGLDEEASGARPPPLIQEHWETVM 435  
Db 541 GTPALETTLTTPPAMAAPKDDGFLNGSCGLDEEASGARPPPLIQEHWETVM 593

RESULT 13  
ABP81872  
ID ABP81872 standard; protein; 593 AA.  
XX  
XX ABP81872;  
XX AC  
XX DT 04-MAR-2003 (first entry)  
XX  
XX Human parathyroid hormone receptor 1 protein SEQ ID NO:229.  
XX  
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
XX G protein-coupled receptor modulator; antibody; immune-related disease;  
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;  
XX immunological-related cell proliferative disease; autoimmune disease;  
XX Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
XX ulcer.  
XX  
XX Homo sapiens.  
XX OS  
XX W0200261087-A2.  
XX  
XX 08-AUG-2002.  
XX  
XX 19-DEC-2001; 2001WO-US050107.  
XX  
XX 19-DEC-2000; 2000US-0257144P.  
XX  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX  
XX Burmer GC, Roush CL, Brown JP;  
XX  
XX WPI; 2003-046718/04.  
XX N-PSDB; ABZ42719.  
XX  
XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
XX (GPCR), useful for diagnosing and designing drugs for treating conditions  
XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
XX autoimmune diseases.  
XX  
XX Disclosure; Fig 1; 523pp; English.  
XX  
XX The present invention describes antigenic peptides (I) comprising: (a)  
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
XX acids. Also described: (1) an assay for the detection of a particular G  
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
XX and (2) an isolated antibody having high specificity and high affinity or  
XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in  
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
XX antibody against a particular GPCR, and in the production of specific  
XX antibodies. The peptides and antibodies are also useful for detecting the  
XX presence or absence of corresponding GPCRs. The antigenic peptides for  
XX GPCRs and antibodies are useful for diagnosing and designing drugs for  
XX treating immune-related diseases, growth-related diseases, cell  
XX regeneration-related disease, immunological-related cell proliferative  
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,  
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, graft versus host  
XX inflammation, allergies, Crohn's disease, diabetes, chronic and acute  
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory  
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
XX any other disorder in which GPCRs are involved. The antibodies may be  
XX used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the  
XX exemplification of the present invention

```
XX SQ Sequence 593 AA;
Query Match      88.0%; Score 2008; DB 6; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.1e-189;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKBEQIFLLHRAQAQCEKRLKEVLQRP 60
QY 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGKLYPESEEDKEAPTGSRYGRPCLPEDHILCWPL 120
QY 26 ----- 25
Db 121 GAPEVVAVPCPDYIDFNHKGHAYRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAVSIFVK 240
QY 85 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEAERLTEBELRAIAQAPPPATAAGYAGCRVAVTFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWVRATLANTGCDLSSGNKK 360
QY 205 WIIQVPILASVVLNFIINIRVLATKLRETNAGRCDTQGYRKLLRSLVLVPLFGVH 264
QY 265 YTVFMALPYTEVSGTLWQIQMHEMLFNSFQGFVAILIYFCNGEVOAEIRKSWRWTIA 324
Db 421 YIVFMATPYTEVSGTLWQVQHEMLFNSFQGFVAILIYFCNGEVOAEIKSWRWTIA 480
QY 325 LDFEKBKSGSSSYSGPMVSHTSVTNVGPRAGLSLPSR-LPPATNGHSQLPFHAKP 383
Db 481 LDFEKBKSGSSSYSGPMVSHTSVTNVGPRVGLPLSPRLLPATNGHPQLFHAKP 540
QY 384 CAPATET-ETLPTVMVAPKDGFLNGSCGLDEEASGARPPPLQEGWETVM 435
Db 541 GTPALETLTETTPMAAPKDDGFLNGSCGLDEEASGPERRPALLOEWETVM 593

RESULT 14
ADE83418
ID ADE83418 standard; protein; 593 AA.
XX AC ADE83418;
XX AC ADE83418;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein Q03431, SEQ ID NO 11013.
XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN W02003016475-A2.
XX XX 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
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XX PA (GEHO ) GEN HOSPITAL CORP.
XX PA (FARB ) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX XX MPI; 2003-268312/26.
XX DR GENBANK; Q03431.
XX XX
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX XX
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a human protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 593 AA;
```

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Query Match      88.0%; Score 2008; DB 7; Length 593;
Best Local Similarity 67.3%; Pred. No. 1.1e-189;
Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;

QY 1 MGAARIAPSLALLCCPVLSSAYAL----- 25
Db 1 MGTARIAPGLALLCCPVLSSAYALVDADDVMTKBEQIFLLHRAQAQCEKRLKEVLQRP 60
QY 26 ----- 25
Db 61 SIMESDKGWTSASTSGKPRKDKASGKLYPESEEDKEAPTGSRYGRPCLPEDHILCWPL 120
QY 26 ----- 25
Db 121 GAPEVVAVPCPDYIDFNHKGHAYRCDRNGSWELVPGHNRTWANYSECVKFLTNETRE 180
QY 26 -EVFDRLGMIYTVGYSMSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAASIFVK 84
Db 181 REVFDRLGMIYTVGYSVSLASLTAVLILAYFRRLHCTRNVIHMHMFLSFMRLRAVSIFVK 240
QY 85 DAVLYSGFTLDEAERLTEBELHIIAQVPPPPAAAAGVAGCRVAVTFFLYFLATNYWIL 144
Db 241 DAVLYSGATLDEAERLTEBELRAIAQAPPPATAAGYAGCRVAVTFFLYFLATNYWIL 300
QY 145 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWVRATLANTGCDLSSGHKK 204
Db 301 VEGLYLHSLIFMAFFSEKKYLWGFTIFGWLPAVFVAVVWVRATLANTGCDLSSGNKK 360
QY 205 WIIQVPILASVVLNFIINIRVLATKLRETNAGRCDTQGYRKLLRSLVLVPLFGVH 264
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Db	361	WIIQVPIIASIVLNFLINIVRVLATKLRETNAGRC	TRQQYRKLRKSTLVLMPLFGVH	420		
Qy	265	YTVFMALPYTEVSGTLWQIQMHEMFLNSFGQFFV	AIYFCNCEVQAEIRKSWSRWTLA	324		
Db	421	YIVFMATPYTEVSGTLWQIQMHEMFLNSFGQFFV	AIYFCNCEVQAEIRKSWSRWTLA	480		
Qy	325	LDFKRRKARGSSSYSGPMVSHTSVTNVGP	RAGLSLPLSPR-LPPATTNGHSQLPGHAKP	383		
Db	481	LDFKRRKARGSSSYSGPMVSHTSVTNVGP	RVLGLPLSPRLPTATTNGHPQLPGHAKP	540		
Qy	384	GAPATET-ETLPTVMAVPKDDGFLNGSCGLDDE	ASGSRPPLLOEGWETVM	435		
Db	541	GTPALETLETTPMAAPKDDGFLNGSCGLDDE	ASGSRPPLLOEGWETVM	593		
RESULT 15						
ADP70390	standard; protein; 593 AA.					
ID	AC	ADF70390;				
XX	12-FEB-2004	(first entry)				
DT	Human PTH-R protein related to orphan receptor ligands.					
XX	ligand; orphan receptor protein; fusion protein; fluorescent protein;					
KW	cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;					
KW	GFPuv; Enhanced GFP; EGFP; human; PTH-R.					
XX	Homo sapiens.					
OS	WO2003071272-A1.					
XX	28-AUG-2003.					
PD	21-FEB-2003; 2003WO-JP001901.					
XX	21-FEB-2002; 2002JP-00045728.					
PR	23-JUL-2002; 2002JP-00213949.					
PR	11-OCT-2002; 2002JP-00298237.					
XX	(TAKE ) TAKEDA CHEM IND LTD.					
PA	Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;					
PI	WPI; 2003-697654/66.					
XX	N-PSDB; ADF70391.					
DR	Transformation of cells with a fusion protein of an orphan receptor					
XX	protein with a fluorescent protein useful for identification of ligands					
PT	to the orphan receptor.					
PS	Example 2; SEQ ID NO 13; 594pp; Japanese.					
XX	This invention relates to a novel method of identifying ligands to an					
CC	orphan receptor protein which comprises transforming cells with DNA					
CC	encoding a fusion protein of the orphan receptor with a fluorescent					
CC	protein, so that the fusion protein is expressed in the cells (or cell					
CC	membranes isolated from them) and contacting the cells with the potential					
CC	ligand to be tested. A suitable fluorescent protein for incorporation in					
CC	the fusion protein is green fluorescent protein (GFP), for example GFP-1,					
CC	wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the					
CC	identification of ligands binding to an orphan receptor protein.					
XX	Sequence 593 AA;					
QY	Query Match 88.0%; Score 2008; DB 7; Length 593;					
XX	Best Local Similarity 67.3%; Pred. No. 1.1e-189;					
XX	Matches 399; Conservative 10; Mismatches 26; Indels 158; Gaps 3;					
QY	1	MGTARIAPGLALLCCPVLSAYALVAD			DVMTKEEQIFLLHRAQCCBKRLKEVLQ	RPA 60
Qy	26	-----	-----	25		
Db	61	SIMESDKWTSASTSGKPRKDKASGLYP	SESEEDKEAPTGSRYGRPCLP	PEWDHILCWPL 120		
Qy	26	-----	-----	25		
Db	121	GAPGEVAVPCDVIYDFNHKHAYRRCD	RNGSWELVPGHNRTWANYSECV	KELTNETRE 180		
Qy	26	-EVDRLGMIYTVGYSMSLASLT	TVAVLILAYFRRLHCTRNYI	HHMFLSPMLRAASIFVK 84		
Db	181	REVDRLGMIYTVGYSVSLASLT	TVAVLILAYFRRLHCTRNYI	HHMFLSPMLRAVSI	FVK 240	
Qy	85	DAVYSGFTLDEABRLTEEBLHII	TAQVPPPPAAAAGVACRVAVT	FFLYFLATNYYWIL 144		
Db	241	DAVLYSGATLDEABRLTEEBLHII	TAQVPPPPATAAAGVACRVAVT	FFLYFLATNYYWIL 300		
Qy	145	VEGLYLHSLIFMAFFSEKKYLWGFT	IFGWGLPAVFVAVVWVGRATL	ANTGCWDLSSGHKK 204		
Db	301	VEGLYLHSLIFMAFFSEKKYLWGFT	IFGWGLPAVFVAVVWVSRATL	ANTGCWDLSSGNKK 360		
Qy	205	WIIQVPIIASIVLNFLINIVRVLATKL	RETNAGRC	TRQQYRKLRKSTLVLMPLFGVH 264		
Db	361	WIIQVPIIASIVLNFLINIVRVLATKL	RETNAGRC	TRQQYRKLRKSTLVLMPLFGVH 420		
Qy	265	YTVFMALPYTEVSGTLWQIQMHEMFL	NSFGQFFVAIIYFCNCEVQAEIR	KSWRWTLA 324		
Db	421	YIVFMATPYTEVSGTLWQIQMHEMFL	NSFGQFFVAIIYFCNCEVQAEIR	KSWRWTLA 480		
Qy	325	LDFKRRKARGSSSYSGPMVSHTSVTN	VGP	RAGLSLPLSPR-LPPATTNGHSQLPGHAKP 383		
Db	481	LDFKRRKARGSSSYSGPMVSHTSVTN	VGP	RVLGLPLSPRLPTATTNGHPQLPGHAKP 540		
Qy	384	GAPATET-ETLPTVMAVPKDDGFLNG	SCGLDDEASGSRPPLLOEGWETVM	435		
Db	541	GTPALETLETTPMAAPKDDGFLNG	SCGLDDEASGSRPPLLOEGWETVM	593		

Search completed: November 23, 2004, 20:57:46  
Job time : 160 secs